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M protein - protein search, using sw model

run on: March 19, 2004, 11:20:21 ; Search time 17.0916 Seconds
(without alignments)
785.341 Million cell updates/sec

title: US-09-989-903-2
perfect score: 1350
sequence: 1 KPDMESEMDPQLOERYD.....KPKVNPVQSTLRKLYLQ 260

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 389414 seqs, 51625971 residues

total number of hits satisfying chosen parameters: 389414

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB pep.*
3: /cgn2_6/ptodata/2/iaa/5A COMB pep.*
4: /cgn2_6/ptodata/2/iaa/6A COMB pep.*
5: /cgn2_6/ptodata/2/iaa/6B COMB pep.*
6: /cgn2_6/ptodata/2/iaa/6C COMB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	260	4	US-09-187-789-2
2	1350	100.0	260	4	US-09-139-600-2
3	934.5	69.2	242	4	US-09-187-789-5
4	804.5	59.6	214	4	US-09-187-789-9
5	692.5	51.3	230	4	US-09-187-789-7
6	384	28.4	74	4	US-09-187-789-63
7	384	28.4	74	4	US-09-139-600-58
8	299	22.1	56	4	US-09-187-789-64
9	299	22.1	56	4	US-09-139-600-59
10	280	20.7	53	4	US-09-187-789-65
11	280	20.7	53	4	US-09-139-600-60
12	275.5	20.4	435	5	PCT-US94-07127A-4
13	274.5	20.3	421	4	US-08-983-502-10
14	274.5	20.3	421	4	US-09-516-747-10
15	274.5	20.3	421	5	PCT-US96-10521-10
16	274.5	20.3	435	3	US-08-258-287B-53
17	274.5	20.3	435	3	US-08-368-704C-51
18	274.5	20.3	435	4	US-09-561-756-9
19	274.5	20.3	435	4	US-09-237-721-9
20	274.5	20.3	435	4	US-08-816-075-2
21	274.5	20.3	435	4	US-08-724-378D-9
22	274.5	20.3	435	4	US-09-954-697-9
23	274.5	20.3	441	3	US-08-258-287B-44
24	274.5	20.3	441	3	US-08-368-704C-43
25	274	20.3	277	2	US-08-890-542A-2
26	274	20.3	277	3	US-08-591-605-2
27	274	20.3	277	3	US-08-964-308-6

28	274	20.3	277	3	US-08-462-969B-4	Sequence 4, Appli
29	274	20.3	277	3	US-08-964-313-6	Sequence 6, Appli
30	274	20.3	277	4	US-09-069-138-6	Sequence 6, Appli
31	274	20.3	277	4	US-09-124-934A-4	Sequence 4, Appli
32	274	20.3	277	4	US-08-334-251D-4	Sequence 4, Appli
33	273	20.2	277	4	US-09-561-756-12	Sequence 12, Appli
34	273	20.2	277	4	US-09-227-721-12	Sequence 12, Appli
35	273	20.2	277	4	US-08-983-502-30	Sequence 30, Appli
36	273	20.2	277	4	US-08-724-378D-5	Sequence 5, Appli
37	273	20.2	277	4	US-09-516-747-30	Sequence 30, Appli
38	273	20.2	277	4	US-09-954-697-12	Sequence 12, Appli
39	273	20.2	277	4	PCT-US96-10521-30	Sequence 30, Appli
40	265	19.6	277	4	US-09-291-289-11	Sequence 11, Appli
41	265	19.6	503	3	US-08-258-287B-36	Sequence 36, Appli
42	265	19.6	503	3	US-08-368-704C-36	Sequence 36, Appli
43	264.5	19.6	435	4	US-09-291-289-10	Sequence 10, Appli
44	264	19.6	277	3	US-08-964-308-10	Sequence 10, Appli
45	264	19.6	277	3	US-08-964-313-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-09-187-789-2

; Sequence 2, Application US/09187789

; Patent No. 6340740

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: CASPAGE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING

; FILE REFERENCE: 480140.434C1

; CURRENT APPLICATION NUMBER: US/09/187,789

; CURRENT FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 260

; TYPE: PRI

; ORGANISM: Mus musculus

; US-09-187-789-2

Query Match 100.0%; Score 1350; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 9.6e-135;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	KPDMESEMDPQLOERYDMSGARLALTCVTKAREGSEVDMSEALRMFRYLKPESTMK	60
Db	1	KPDMESEMDPQLOERYDMSGARLALTCVTKAREGSEVDMSEALRMFRYLKPESTMK	60
Qy	61	RDPTAQFLLEELDEFQOTIDNWEPPVSCAFVVMAGBEGLLKGEDEKXVRLEDLFEVLN	120
Db	61	RDPTAQFLLEELDEFQOTIDNWEPPVSCAFVVMAGBEGLLKGEDEKXVRLEDLFEVLN	120
Qy	121	NKCKALRGKPKYIIQACRGEHRDPGEELRNEELGGDEELGGDEAVLKNPQISITY	180
Db	121	NKCKALRGKPKYIIQACRGEHRDPGEELRNEELGGDEELGGDEAVLKNPQISITY	180
Qy	181	TDTHIYSTVEGVLVSRHDEKSGGFIQTLDVPIHKKGSIILTEITRLMANTVWQEG	240
Db	181	TDTHIYSTVEGVLVSRHDEKSGGFIQTLDVPIHKKGSIILTEITRLMANTVWQEG	240
Qy	241	KPKVNPVQSTLRKLYLQ	260
Db	241	KPKVNPVQSTLRKLYLQ	260

RESULT 2

US-09-139-600-2

; Sequence 2, Application US/09139600

; Patent No. 6432628

; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
S-09-139-600-2

Query Match 100.0%; Score 1350; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 9.6e-135; Indels 0; Gaps 0;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 KPMSEMSDPPQLOERYDMSGARLALTLCTVKAREGSEVDMEALERNFRLKFESTMK 60
b 1 KPMSEMSDPPQLOERYDMSGARLALTLCTVKAREGSEVDMEALERNFRLKFESTMK 60
Y 61 RDPTAQOFLDEFOOTIDNNEEPVSCAFVVLMAHGEGLLKGDEKXVLEDLFEVLN 120
b 61 RDPTAQOFLDEFOOTIDNNEEPVSCAFVVLMAHGEGLLKGDEKXVLEDLFEVLN 120
Y 121 NKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDEVAVLKNPQSIPTY 180
b 121 NKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDEVAVLKNPQSIPTY 180
Y 181 TDTLHIYSTVEGYSYRHDKSGSGFIQTLTDVFIHKGSILELTTETRLMANTVWQEG 240
b 181 TDTLHIYSTVEGYSYRHDKSGSGFIQTLTDVFIHKGSILELTTETRLMANTVWQEG 240
Y 241 KPRKVNPEVQSTLRKXLYLQ 260
b 241 KPRKVNPEVQSTLRKXLYLQ 260

RESULT 3
S-09-187-789-5
Sequence 5, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
S-09-187-789-5

Query Match 69.2%; Score 934.5; DB 4; Length 242;
Best Local Similarity 70.9%; Pred. No. 8.7e-91;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
Y 8 MSDPQLOERYDMSGARLALTLCTVKAREGSEVDMEALERNFRLKFESTMKRDPTAQQ 67
b 1 MSNPRSEEEKYDMSGARLALTLCTVKAREGSEVDMEALERNFRLKFESTMKRDPTAQQ 60
Y 68 FLEELDEFQOTIDNNEEPVSCAFVVLMAHGEGLLKGDEKXVLEDLFEVLNKNCKAL 127
b 61 FQEELEKFOQALDSREDPVSCAFVVLMAHGEGLLKGDEKXVLEDLFEVLNKNCKAL 120
Y 128 RGPVKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDEVAVLKNPQSIPTYTDLHI 186

Db 121 RAKPKVYIIQACRGEHRDPG-----ETVGGDEIVVMVKDSPTIPTYTDLHV 168
QY 187 YSTVEGYLSYRHDKSGSGFIQTLTDVFIHKGSILELTTETRLMANTVWQEGKPKVN 246
Db 169 YSTVEGYIAYRHDQKSGCFIQTLDVDFTKRGHILELLTEVTRMAEALVQEGKARKTN 228
QY 247 PEVQSTLRKXLYLQ 260
Db 229 PEIQSTLRKRLYLQ 242

RESULT 4
US-09-187-789-9
Sequence 9, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-9

Query Match 59.6%; Score 804.5; DB 4; Length 214;
Best Local Similarity 63.0%; Pred. No. 4.2e-77;
Matches 160; Conservative 27; Mismatches 26; Indels 41; Gaps 3;
QY 8 MSDPQLOERYDMSGARLALTLCTVKAREGSEVDMEALERNFRLKFESTMKRDPTAQQ 67
Db 1 MSNPRSEEEKYDMSGARLALTLCTVKAREGSE----- 34
QY 68 FLEELDEFQOTIDNNEEPVSCAFVVLMAHGEGLLKGDEKXVLEDLFEVLNKNCKAL 127
Db 35 --ELEEKFOQALDSREDPVSCAFVVLMAHGEGLLKGDEKXVLEDLFEVLNKNCKAL 92
QY 128 RGPVKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDEVAVLKNPQSIPTYTDLHI 186
Db 93 RAKPKVYIIQACRGEHRDPG-----ETVGGDEIVVMVKDSPTIPTYTDLHV 140
QY 187 YSTVEGYLSYRHDKSGSGFIQTLTDVFIHKGSILELTTETRLMANTVWQEGKPKVN 246
Db 141 YSTVEGYIAYRHDQKSGCFIQTLDVDFTKRGHILELLTEVTRMAEALVQEGKARKTN 200
QY 247 PEVQSTLRKXLYLQ 260
Db 201 PEIQSTLRKRLYLQ 214

RESULT 5
US-09-187-789-7
Sequence 7, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 230

```
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-7

Query Match      51.3%; Score 692.5; DB 4; Length 230;
Best Local Similarity 72.0%; Pred. No. 3.4e-65;
Matches 134; Conservative 22; Mismatches 17; Indels 13; Gaps 2;

QY 8 MSDPQLOEERYDMSGARLALTLCTVKAREGSEVDMALERMRYLKPFSTMKRDPDPAQ 67
DB 1 MENPSLEEKYDMSGARLALTLCTVKAREGSEDDLALEHMFQRLFSTMKRDPDPAQ 60
QY 68 FLEELDEFQQTIDNWEFVSCAFVVLMAHGBEGLLKGDEKMLELDFEVLNNKCKAL 127
DB 61 FQEELEKQQAIDSRDFVSCAFVVLMAHGBEGLLKGDEKMLELDFEVLNNKCKAL 120
QY 128 RQPKVYIIQACRGHHRDPGSELGRNVEELGGDEBELGGDE-VAVLKNPQSIPTTDLHI 186
DB 121 RAKPKVYIIQACRGHHRDPG-----ETVGGDEIVVVIKQSPQTIPTTDLHV 168
QY 187 YSTVEG 192
DB 169 YSTVEG 174

RESULT 6
US-09-187-789-63
; Sequence 63, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-63

Query Match      28.4%; Score 384; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.9e-33;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AREGSEVDMALERPRYLKPFSTMKRDPDPAQFLEELDEFQQTIDNWEFVSCAFVVL 94
DB 1 AREGSEVDMALERPRYLKPFSTMKRDPDPAQFLEELDEFQQTIDNWEFVSCAFVVL 60
QY 95 AHGEGLLKGEDEK 108
DB 61 AHGEGLLKGEDEK 74

RESULT 7
US-09-139-600-58
; Sequence 58, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-58

Query Match      22.1%; Score 299; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MYRLDLEFVLNNKCKALRGKPKVYIIQACRGHHRDPGSELGRNVEELGGDEELGG 164
DB 1 MYRLDLEFVLNNKCKALRGKPKVYIIQACRGHHRDPGSELGRNVEELGGDEELGG 56

RESULT 8
US-09-187-789-64
; Sequence 64, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-64

Query Match      22.1%; Score 299; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MYRLDLEFVLNNKCKALRGKPKVYIIQACRGHHRDPGSELGRNVEELGGDEELGG 164
DB 1 MYRLDLEFVLNNKCKALRGKPKVYIIQACRGHHRDPGSELGRNVEELGGDEELGG 56

RESULT 9
US-09-139-600-59
; Sequence 59, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-59

Query Match      22.1%; Score 299; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MYRLDLEFVLNNKCKALRGKPKVYIIQACRGHHRDPGSELGRNVEELGGDEELGG 164
DB 1 MYRLDLEFVLNNKCKALRGKPKVYIIQACRGHHRDPGSELGRNVEELGGDEELGG 56
```

db 1 MVRLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGG 56

RESULT 10

Sequence 65, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 65
LENGTH: 53
TYPE: PRT
ORGANISM: Mus musculus
JS-09-187-789-65

Query Match 20.7%; Score 280; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e-22;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 165 DEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIHKK 217
|||||
db 1 DEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIHKK 53
|||||

RESULT 11

Sequence 60, Application US/09139600
Patent No. 6432628
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHOD OF USE
FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
LENGTH: 53
TYPE: PRT
ORGANISM: Mus musculus
JS-09-139-600-60

Query Match 20.7%; Score 280; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e-22;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 165 DEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIHKK 217
|||||
b 1 DEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIHKK 53
|||||

RESULT 12

CT-US94-07127A-4
Sequence 4, Application PC/TUS9407127A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Interleukin-1 Converting Enzyme Like Apoptosis Protease-1, an
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND

STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07127A
FILING DATE: submitted herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR 2
MOLECULE TYPE: PROTEIN
PCT-US94-07127A-4

Query Match 20.4%; Score 275.5; DB 5; Length 435;
Best Local Similarity 29.6%; Pred. No. 1.3e-20;
Matches 68; Conservative 53; Mismatches 100; Indels 9; Gaps 4;

Qy 36 REGSEVDMEALERMFYLLKFESTMKRDPDTAQOFLFELDFEFOQTIDNNEEPVSCAFVILMA 95
|||
Db 202 RSGGDVDSHTLTLFLKLGVDVHVLCDQTAGEKEKLNFAQ-LPAHRVTDSC-IVALLS 259
|||
Qy 96 HGEGLLKGEDEKMWRLDELFEVLANNKCKALRGKPKVYIIQACRGEHRDPGEELRGNEE 155
|||
Db 260 HGVEGAIYGVGDKLQLQEVFOLFNDNANCPSLQNKPMFFQACRGETDRGVQDQGN 319
|||
Qy 156 LGGDEBELGGDEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIH 215
|||
Db 320 HAGSPCEESDAGKEKLPKMRDLPTRSDMICGYACLGTAAMNTRGSGWYEAQAQVF-S 378
|||
Qy 216 KXGSILELTFEITRLMANTVYMQEKKP-----KVNPEVQSTLRKKLYL 259
|||
Db 379 ERGCDMHVADMLVKVNALIKDREGVAPGTGFHRCCKEMSEYCGSTLCRHYL 428
|||

RESULT 13

US-08-983-502-10
Sequence 10, Application US/08983502
Patent No. 6399327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Yuri V. GOLTSSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-502-10

Query Match 20.3%; Score 274.5; DB 4; Length 421;
Best Local Similarity 29.7%; Pred. No. 1.6e-20;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;
QY 36 REGSEVDMEALERMFYKLPSTMKRDPDTAQOFLBELDEFQQTIDNWEPEVSCAFVVLMA 95
Db 188 RSGGDVHSTLTFLKLGVDVHVLCDTAQEMQEKLNFAQ-LPAHRTDSC-IVALLS 245
QY 96 HGEGLLKGEDEKVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGELRGNEE 155
Db 246 HGVEGAIYGVGDKLLQLOEVFQFNANCPSLQNKPKMFFIQAQCRGDETDGRVDQDQGN 305
QY 156 LGGDEELGDEVAVLKNNPQSIPTVTDTHIYSTVEGYSVRHDEKSGFTQTLTDVFIH 215
Db 306 HAGSPCEESDAGKELPKMRLPTRSDMICGYACLKGTAAAMNTKRGSWYIEALAQVFE 365
QY 216 KGGS--ILELTEITRLMANTVMOEGKP---RKNPEVQSTLRKLYL 259
Db 366 RACDMHVADMLVKVNALIKDREGYAPGTFFHRCKEMSEYCSLTCRHLYL 414

RESULT 14
US-09-516-747-10
Sequence 10, Application US/09516747
Patent No. 6586571
GENERAL INFORMATION:
APPLICANT: David WALLACH
Mark P. BOLDIN
Tanya M. GONCHAROV
Yury V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,747
FILING DATE: 01-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/983,502
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-516-747-10

Query Match 20.3%; Score 274.5; DB 4; Length 421;
Best Local Similarity 29.7%; Pred. No. 1.6e-20;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;
QY 36 REGSEVDMEALERMFYKLPSTMKRDPDTAQOFLBELDEFQQTIDNWEPEVSCAFVVLMA 95
Db 188 RSGGDVHSTLTFLKLGVDVHVLCDTAQEMQEKLNFAQ-LPAHRTDSC-IVALLS 245
QY 96 HGEGLLKGEDEKVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGELRGNEE 155
Db 246 HGVEGAIYGVGDKLLQLOEVFQFNANCPSLQNKPKMFFIQAQCRGDETDGRVDQDQGN 305
QY 156 LGGDEELGDEVAVLKNNPQSIPTVTDTHIYSTVEGYSVRHDEKSGFTQTLTDVFIH 215
Db 306 HAGSPCEESDAGKELPKMRLPTRSDMICGYACLKGTAAAMNTKRGSWYIEALAQVFE 365
QY 216 KGGS--ILELTEITRLMANTVMOEGKP---RKNPEVQSTLRKLYL 259
Db 366 RACDMHVADMLVKVNALIKDREGYAPGTFFHRCKEMSEYCSLTCRHLYL 414

RESULT 15
PCT-US96-10521-10
Sequence 10, Application PC/TUS9610521
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34

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/ NUMBER OF SEQUENCES: 34
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/10521
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 114,615
/ FILING DATE: 16-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 114,986
/ FILING DATE: 17-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 115,319
/ FILING DATE: 14-SEP-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 116,588
/ FILING DATE: 27-DEC-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 117,932
/ FILING DATE: 16-APR-1996
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 421 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ CT-US96-10521-10

Query Match      20.3%; Score 274.5; DB 5; Length 421;
Best Local Similarity 29.7%; Pred. No. 1.6e-20;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;

2Y 36 REGSEVDMEALERMFYLFKESTWKRDPDTAQQLFELDEPQQTIDNWEEFVSCAFVILMA 95
Db 188 RSGGDVDHSTLVTLFGLGVDVHVLCDTAQEMQEKLNQPAQ-LPAHRVTDSQ-IVALLS 245
2Y 96 HGEGLLKGEDEKMRLEDLFVLNNKNKALRGKPKYIIQACRGEHRDPGEELRGNEE 155
Db 246 HGEVGIYGVGKLLQLEVFQLFQFNANCPSLQNKPKMPFIQACRGDETDGRGVDDQDGKN 305
2Y 156 LGDBELGSDDEVAVLKNPQSIPTTYDTLHIYSTVEGYLSYRDEKSGSFIQTLDVFIH 215
Db 306 HAGSPGCEESDAGKEKLPKMRPLTRSDMICGYACLKGTAMRNTRKGSWYIEALAQVFSE 365
2Y 216 KKGS--ILELTEEITRLMANTENVQEGKP---RKNVPEVQSTLRKKLYL 259
Db 366 RACDMHVADMLVKVNAIJKDEGVAPGTETFRCKEMSEYCVSTLCRHLYL 414
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Search completed: March 19, 2004, 11:25:36
Job time : 18.0916 secs

GenCore version 5.1.6
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* protein - protein search, using sw model

on on: March 19, 2004, 11:17:55 ; Search time 37.2908 seconds

(without alignments)
2199.863 Million cell updates/sec

itle: US-09-989-903-2

erfect score: 1350

equences: 1 KPDMESEMSDQPLQERYD.....KPRKVNPEVQSLTKKLYLQ 260

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

earched: 1017041 seqs, 315518202 residues

otal number of hits satisfying chosen parameters: 1017041

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriopl.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	235.5	21.9	423	Q91B67	Q91B67 xenopus lae
2	279.5	20.7	452	Q8C9H7	Q8C9H7 mus musculus
3	278	20.6	318	Q91B65	Q91B65 xenopus lae
4	278	20.6	403	Q90WU0	Q90WU0 gallus gall
5	277	20.5	277	Q8MJU1	Q8MJU1 felis silve
6	276.5	20.5	452	Q8K241	Q8K241 mus musculus
7	276	20.4	313	Q8CHV5	Q8CHV5 mus musculus
8	274.5	20.3	435	Q9BUP7	Q9BUP7 homo sapien
9	274.5	20.3	452	Q55194	Q55194 rattus norv
10	273	20.2	277	Q95ND5	Q95ND5 sus scrofa
11	270.5	20.0	277	Q8MKI5	Q8MKI5 canis faml
12	266	19.7	277	Q8MJC3	Q8MJC3 oryctolagus
13	266	19.7	282	Q98UI8	Q98UI8 brachydanio
14	266	19.7	454	Q9R0T0	Q9R0T0 mus musculus
15	264.5	19.6	303	Q88550	Q88550 rattus norv
16	263	19.5	453	Q8C3Q0	Q8C3Q0 mus musculus

17	263	19.5	454	11	Q8C3Q9	Q8C3Q9 mus musculus
18	261.5	19.4	316	5	Q8I7B0	Q8I7B0 geodia cydo
19	261.5	19.4	426	5	Q8I6Y2	Q8I6Y2 geodia cydo
20	255	18.9	454	11	Q90HK1	Q90HK1 rattus norv
21	254	18.8	399	13	Q91B63	Q91B63 xenopus lae
22	253	18.7	280	13	Q8JIS9	Q8JIS9 oryzias lat
23	253	18.7	283	13	Q93417	Q93417 gallus gall
24	253	18.7	289	5	Q86PU0	Q86PU0 anopheles s
25	252	18.7	302	13	Q91B89	Q91B89 oncorhynch
26	250	18.5	280	13	Q8JCM9	Q8JCM9 fugu rubrip
27	250	18.5	290	13	Q8UIS8	Q8UIS8 oryzias lat
28	249	18.4	280	13	Q8UG42	Q8UG42 fugu rubrip
29	246	18.2	182	6	O77623	O77623 ovis aries
30	245.5	18.2	476	13	Q91B73	Q91B73 brachydanio
31	241.5	17.9	328	5	Q8ITP3	Q8ITP3 branchiosto
32	241	17.9	304	13	Q93415	Q93415 gallus gall
33	241	17.9	482	11	Q9JHX4	Q9JHX4 rattus norv
34	240.5	17.8	520	13	Q91B62	Q91B62 xenopus lae
35	238	17.6	417	5	Q91IU6	Q91IU6 pristionchu
36	237	17.6	276	11	Q9D089	Q9D089 mus musculu
37	236.5	17.5	293	5	Q8I9V7	Q8I9V7 bombyx mori
38	236	17.5	189	11	Q8BNT4	Q8BNT4 mus musculu
39	234.5	17.4	482	13	Q90WU1	Q90WU1 gallus gall
40	234	17.3	276	11	Q9M47	Q9M47 mus musculu
41	233.5	17.3	277	11	Q35397	Q35397 rattus norv
42	232	17.2	383	13	Q919L7	Q919L7 brachydanio
43	232	17.2	415	13	Q801M6	Q801M6 xenopus lae
44	229	17.2	419	13	Q7ZXD2	Q7ZXD2 xenopus lae
45	229	17.0	283	13	O42284	O42284 gallus gall

ALIGNMENTS

RESULT 1

Q91B67	PRELIMINARY;	PRT;	423 AA.
ID	Q91B67		
AC	Q91B67		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Caspase-2.		
GN	XCASPAGE-2.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20209426; PubMed=10744739;		
RA	Nakajima K., Takahashi A., Yaoita Y.;		
RT	"Structure, expression and function of the Xenopus laevis caspase		
RT	family.";		
RL	J. Biol. Chem. 275:10484-10491 (2000).		
DR	EMBL; AB038168; BAA94746.1; -		
DR	HSSP; P29466, LICE.		
DR	MEROPS; C14.006; -		
DR	GO; GO:0005622; C:intracellular; IEA.		
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.		
DR	GO; GO:0030693; F:caspase activity; IEA.		
DR	GO; GO:0006915; P:apoptosis; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001315; CARD.		
DR	InterPro; IPR002138; ICE_p10.		
DR	InterPro; IPR001309; ICE_p20.		
DR	InterPro; IPR002398; Peptidase_C14.		
DR	Pfam; PF00619; CARD; 1.		
DR	Pfam; PF00656; Peptidase_C14; 1.		
DR	PRINTS; PR00376; IL1BCENZME.		
DR	SMART; SM00114; CARD; 1.		
DR	SMART; SM00115; CASC; 1.		
DR	PROSITE; PS50209; CARD; 1.		

R PROSITE; PS01122; CASPASE_CYS; 1.
 R PROSITE; PS01121; CASPASE_HIS; 1.
 R PROSITE; PS0207; CASPASE_P10; 1.
 R PROSITE; PS0208; CASPASE_P20; 1.
 Q SEQUENCE 423 AA; 47123 MW; E31EB1FD133F01FD CRC64;
 Query Match 21.9%; Score 295.5; DB 13; Length 423;
 Best Local Similarity 27.0%; Pred. No. 4.5e-17;
 Matches 84; Conservative 58; Mismatches 104; Indels 65; Gaps 10;
 Y 2 PMESEMDDP-----OPLQERYDMSGARLALTLIC-----VTKARE----- 37
 b 114 PQESTLSRPGRCQICREYRESIDGGPVTVQLCSVNFVTHCOAYKWHSCPRGRALL 173
 Y 38 -----GSEVDMEALERNFRYLKPESTMKRDPDTAQOFLBELDEFOOTIDNW 82
 b 174 ISNVKFPDPDLYRCGGEVDLASLEKLFSLGQYQVDRCLNAQSMNSQLGAFSAL----- 229
 Y 83 BEPVSCAF-----VVLMAHGEGLIKGEDEKMWRLDLFEVLNNKNCALRGPKVYIIQA 138
 b 230 --PVHSALDSCVALLSHGLDGVYTDGLVQLQEVFTALDNAHCPQLONKPKFFIQA 287
 Y 139 CRGEHRDGEELRNEELGG-----DEELGGDEVALVKNPQSIPTVTTTLHIYSTVEGY 193
 b 288 CRGETDRGVDRDGRGQSGSPGCEQSDAGREDIKV-----RLPTQSDMICAYACLKGT 341
 Y 194 LSYRDEKSGSFIQTLTDVFI-HKKGK--ILELTEEITRLMANTENVQEGK---RKVNPE 248
 b 342 VSLRNTKGSWFQDLYSVFSQHSKDTHVADMLVKYNALIKEREHGFCTEHRCKENSE 401
 Y 249 VQSTLRKKLYL 259
 b 402 YCSTLCRDLYL 412

RESULT 2
 Q8C9H7 PRELIMINARY; PRT; 452 AA.
 D Q8C9H7
 C Q8C9H7
 T 01-MAR-2003 (Tremblrel. 23, Created)
 T 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 T 01-OCT-2003 (Tremblrel. 23, Last annotation update)
 DE Caspase 2.
 IN CASP2.
 XS Mus musculus (Mouse).
 XC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 XC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 XX NCBI_TaxID=10090;
 XN [1]
 SEQUENCE FROM N.A.
 IC STRAIN=C57BL/6J; TISSUE=Thymus;
 IC MEDLINE=22354683; PubMed=12466851;
 XA The FANTOM Consortium,
 IA the RIKEN Genome Exploration Research Group Phase I & II Team;
 IT "Analysis of the mouse transcriptome based on functional annotation of
 IT 60,770 full-length cDNAs";
 IL Nature 420:563-573(2002).
 RL EMBL; AK042072; BAC31153.1; -.
 JR MGD; MGI:97295; Casp2.
 JR GO; GO:0005622; C:intracellular; IEA.
 JR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 JR GO; GO:0030693; F:caspase activity; IEA.
 JR GO; GO:0006915; P:apoptosis; IEA.
 JR GO; GO:0006588; P:proteolysis and peptidolysis; IEA.
 JR InterPro; IP001315; CARD.
 JR InterPro; IP002138; ICE_P10.
 JR InterPro; IP001309; ICE_P20.
 JR InterPro; IP002398; Peptidase_C14.
 JR Pfam; PF00619; CARD; 1.
 JR Pfam; PF00656; Peptidase_C14; 1.
 JR PRINTS; PR00376; ILIBCENZYME.
 JR SMART; SM00114; CARD; 1.
 JR SMART; SM00115; CARD; 1.

DR PROSITE; PS0209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS0208; CASPASE_P20; 1.
 SQ SEQUENCE 452 AA; 50889 MW; C3715908508619CA CRC64;
 Query Match 20.7%; Score 279.5; DB 11; Length 452;
 Best Local Similarity 31.0%; Pred. No. 1.2e-15;
 Matches 72; Conservative 52; Mismatches 95; Indels 13; Gaps 6;
 QY 36 RGSVDMEALERNFRYLKPESTMKRDPDTAQOFLBELDEFOOTIDNWEEPVSCAFVILNA 95
 Db 219 RSGVDVHTLVTFRLLGYNVHLVHDTAQEQEKLQNFQA--LPAHRYTDSV--VALLS 276
 QY 96 HGEGLLKGEDEKMWRLDLFEVLNNKNCALRGPKVYIIQACRGEHRDPG---EELRG 152
 Db 277 HGVGGIGVGDGKLLQEQEVPRFLFDNANCPSLQNKPKMFFIQAQCRGDETRDGVQDQDGN 336
 QY 153 NEELGGDEELGGDEVALVKNPQSIPTVTTTLHIYSTVEGYLSYRDEKSGSFIQTLTDV 212
 Db 337 HQSPGCEESDAGKEELMK---MLPTRSDMIQYACLKGNAMRNTRKGSWYIEALTQV 393
 QY 213 FHKKGK--ILELTEEITRLMANTENVQEGK---RKVNPEVQSTLRKKLYL 259
 Db 394 FSEACDMHVDMLVKYNALIKEREHGFCTEHRCKENSEYCSITLCCQLYL 445
 RESULT 3
 Q9IB65 PRELIMINARY; PRT; 318 AA.
 AC Q9IB65
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Caspase-7.
 GN XCASPASE-7.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 CX NCBI_TaxID=8155;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20209426; PubMed=10744739;
 RX Nakajima K., Takahashi A., Yacita Y.;
 RT Structure, expression and function of the Xenopus laevis caspase
 RT family";
 RL J. Biol. Chem. 275:10484-10491(2000).
 DR EMBL; AB038170; BAA94748.1; -.
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.004; -.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IP002138; ICE_P10.
 DR InterPro; IP001309; ICE_P20.
 DR InterPro; IP002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBCENZYME.
 DR SMART; SM00115; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS0208; CASPASE_P20; 1.
 SQ SEQUENCE 318 AA; 35937 MW; 6EBC6684AF6A128 CRC64;
 Query Match 20.6%; Score 278; DB 13; Length 318;
 Best Local Similarity 32.9%; Pred. No. 9.9e-16;
 Matches 77; Conservative 39; Mismatches 96; Indels 22; Gaps 7;
 QY 35 AREGSEVDMEALERNFRYLKPESTMKRDPDTAQOFLBELDEFOOTIDNWEEPVSCAFV-VL 93
 Db 97 ARNGTDIDARELLRCFKGLGFDVNVNKNKSC---EEMENLRTVAQDQDHSACFACIF 152

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151 151 -----RGNEELGGDEELGDEVAVLKNNPQSIPTTDTLHIYST 189
289 289 SPQDETCRSIESDAIPFOAPSGNE---DEP---DAVA-----SLTPGDIIVSYST 334
190 190 VEGYLSYRDEKSGSFIQTLTDFVTHKKGSIILELTEEITRLMANTEVNVQEGKPKRKNPEV 249
335 335 PFGFVSWRKVSGSVETLDSVLEHYARS-----EDLTUKLRLVSDIVSSKGRYKQIPGC 390
250 250 QSTRKXLY 258
391 391 FNFELRKXIF 399

RESULT 5
Q8MJU1 PRELIMINARY; PRT; 277 AA.
ID Q8MJU1 AC Q8MJU1
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Caspase3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki J., Sano J., Kano R., Hasegawa A.;
RT "Felis catus mRNA for caspase3, complete cds.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB090246; BAC10589.1;
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR PROSITE; PS02029; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31465 MW; 8749679C30AB46F6 CRC64;

Query Match 20.5%; Score 277; DB 6; Length 277;
Best Local Similarity 30.5%; Pred. No. 1e-15;
Matches 84; Conservative 40; Mismatches 105; Indels 46; Gaps 9;

QY 6 SEMSDPQLOEERYDMSGARLALTLCVTK-----ARGSEVDMEALERMFRYLFK 55
DB 24 SKMSDGIYMDNSYKMDYPMGLCIINNNKNFHESTGMPFSRGTDVDAANRETFTNLKY 83
QY 56 ESTWKRPDTAQQLLELDEFQQTIDNWERPVSCAFVVLMAHGEGLLKGEDEKMWLEDL 115
DB 84 EVRNKDLTREQIVALLDSVSRDHKRSFPC---VLSHGEELIYGTNGP-VDLKX 139
QY 116 FEVLNNKNCALRGKPKVYIIQACRGEHRDPGSELNGNEELGGDEELGDEVAVLKNNPQ 175
DB 140 TGFFRGDYCRSLTKGPKLFIQACRGTELDGCIETDSGTE-----DDIAC-----Q 185
QY 176 SIPTTDTLHIYSTVEGYLSYRDEKSGSFIQTLTDFVTHKKGSIILELTEEITRLMA 232
DB 186 KIPVEADFLAYSTAPGYYSWRNKSQGSWFIQSLCMLRYAHE-----LEFMILTRV-- 239
QY 233 NTEVMQEGKP-----RKVNPEVOSTLRKKLY 258
DB 240 NRKATEFESFSLDSAFHGKQKQIPCIIVSLTKELY 274

RESULT 6
Q8K241
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94 94 MAMGEELGKGEDEKMWLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGSELGN 153
153 153 LSHGEELIYGTNGP-PIKVLTTLRGDCNCSLVGKPKLFIQACRGEHFDG----- 205
154 154 EEELGGDEELGDEVAVLKNNPQSIPTTDTLHIYSTVEGYLSYRDEKSGSFIQTLTDFV 213
206 206 --LEADSGSVNDSLETDPANRHKIPVEADFLAYSTVPGYYSWRNPFMGSGNFWQALCSV- 262
214 214 IHKKGSIILELTEEITR---LMANTEVNVQEGK---RKVNPEVOSTLRKKLYQ 260
263 263 LNEYGKELEVNQILTRVNFVAIQFESYSDDPFSKXKQIPCVWSMLTKELYFK 316

RESULT 4
Q90WU0 PRELIMINARY; PRT; 403 AA.
ID Q90WU0 AC Q90WU0
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Banton S., Bridgman J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057940; AAL23701.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0016329; P:apoptosis regulator activity; IEA.
DR GO; GO:0005488; P:binding; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR PROSITE; PS02029; MITOCH_CARRIER; 1.
FT NON_TER
SQ SEQUENCE 403 AA; 44913 MW; 0F1E40C3E6594FC4 CRC64;

Query Match 20.6%; Score 278; DB 13; Length 403;
Best Local Similarity 28.2%; Pred. No. 1.4e-15;
Matches 87; Conservative 44; Mismatches 106; Indels 72; Gaps 9;

QY 1 KPDMSEMSDPPQLOEERYDMSGARLALTLCV-----TYAREGSE 40
DB 112 QPESERFRMPAPAGSVAQSDKSRPTDNCSTCEQTPCGHCLIFNNVSFRSDLSSTRAGSD 171
QY 41 VQMEALERMFRYLFKSTWKRPDTAQQLLELDEFQQTIDNWERPVSCAFVVLMAHGEEL- 99
DB 172 IDCEKLEKFRSLCFHVTRLNLKQAEIDVLRKLAR-LDH--SALDCCLVILSHGCGT 228
QY 100 -----GLLKGEDEKMWLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGSEL--- 150
DB 229 SHIQFPGGIYGTGDKTIPIERIVNVYFNFGSQPSLRGKPKLFIQACGGEKQDQGFVDCE 288
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Q8K241 PRELIMINARY; PRT; 452 AA.
Q8K241;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Caspase 2.
CASP2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
Straussberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC034262; AAH34262.1; -.
MGD; MGI:97295; Casp2.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0030693; F:caspase activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006508; P:apoptosis and peptidolysis; IEA.
InterPro; IPR001315; CARD.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASc; 1.
PROSITE; PS02029; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS02027; CASPASE_P10; 1.
PROSITE; PS02028; CASPASE_P20; 1.
SEQUENCE 452 AA; 50661 MW; A4DE25A712FAB855 CRC64;

Query Match 20.5%; Score 276.5; DB 11; Length 452;
Best Local Similarity 30.6%; Pred. No. 2.1e-15;
Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

1Y 36 REGSEVDMEALERFRYLKPESTMKRDPDPTAQOFLBELDFQQTIDNWEFVSCAFVILMA 95
1b 219 RSGGDVHTTIVTLFKLLGYNVHLDQTAQEQKLNFAQ-LPAHRVTDSCV-VALLS 276
1Y 96 HGEGLKGEDEKVRLEDFEVLNNKNCALRGKPVYIIQACRGEHRDPG---BELRG 152
1b 277 HGVEGGYGVGDKLQIQEVRFLDNANCPFLQNKPKMFFIQACRGEHTRDGVQDQGN 336
1Y 153 NEELGGDEELGGDEAVLKNPNQSIPTVDTLHIYSTVEGYLSYRHKDEKSGFIQTLDV 212
1b 337 HTQSPGCEESDAGEELMK---NRLPTRSDMIGYACIKGNAMNTKSGSYIALTVQV 393
1Y 213 FTHKKS--ILETTEITRLMANTVMEQEK---RKVNPEVOSTLRKKLYL 259
1b 394 PSEACDMHVDMLVKVNLIKEREYAPGTGFEHRCKEMSEYCVSTLCQQLYL 445

RESULT 7
8CHV5 PRELIMINARY; PRT; 313 AA.
8CHV5;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Caspase 3, apoptosis related cysteine protease (Fragment).
CASP3.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
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RP SEQUENCE FROM N.A.
RC STRAIN-FV3/N;
RA Straussberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038825; AAH38825.1; -.
DR MGD; MGI:107739; Casp3.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:apoptosis and peptidolysis; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
KW Protease.
FT NON_TER 1
SQ SEQUENCE 313 AA; 35174 MW; 96E98A1F04E769FC CRC64;

Query Match 20.4%; Score 276; DB 11; Length 313;
Best Local Similarity 33.3%; Pred. No. 1.4e-15;
Matches 79; Conservative 39; Mismatches 81; Indels 38; Gaps 9;

QY 35 AREGSEVDMEALERFRYLKPESTMKRDPDPTAQOFLBELDFQQTIDNWEFVSCAFV-VL 93
Db 99 SRSGTDVDAANLRRETFMGLKYQVRNKNDLTREDILELMD----SVSKEDSKRSSFVCVI 154
QY 94 MAHGEGLLKGEDEKVRLEDFEVLNNKNCALRGKPVYIIQACRGEHRDPGEELRGN 153
Db 155 LSHGDEGVIYGTNGP-VELKLTSTFRGDCYCRSLTGKPKLFIQACRGTDLDCGIE---- 209
QY 154 BELGGDEELGGDEAVLKNPNQSIPTVDTLHIYSTVEGYLSYRHKDEKSGFTQTLTD-- 211
Db 210 TDSGTDEEMA-----CQKIPVEADFLYASTAPGYYSWRNSKDGSMFIQSLCSML 259
QY 212 -VFTHKKSILETTEITRLMANTVMEQEK-----PRKVNPEVOSTLRKKLY 258
Db 260 KUYAHK----LEFMILTRV--NRKVATEFESFLDSTFHAKKQIPCIIVSMLTKEY 310

RESULT 8
Q9BUP7 PRELIMINARY; PRT; 435 AA.
Q9BUP7;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to caspase 2 (Neural cell expressed, developmentally
down-regulated 2).
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP Straussberg R.;
RC TISSUE=Skin;
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator (TM) System Donor
vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002427; AAH02427.1; -.
DR EMBL; BT007240; AAP35904.1; -.
DR HSSP; P29466; IICE.
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RR HSP; P29466; ICE.
RR GO; GO:0005622; C:intracellular; IEA.
RR GO; GO:0016329; F:apoptosis regulator activity; IEA.

RESULT 10
O95ND5

RESULT 10
Q95ND5 PRELIMINARY; PRT; 277 AA.
ID Q95ND5
AC Q95ND5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1] _
RN SEQUENCE FROM N.A.
RP MEDLINE=213334413; PubMed=11440638;
RX Muneta Y., Shimojima Y., Mori Y.:
RA "Porcine caspase-3: cloning and its activity during apoptosis of
RT porcine PK15 cells induced by porcine Fas-ligand.";
RL J. Interferon Cytokine Res. 21:409-415(2001).
RR EMBL; AB029345; BAB55544.1; --
DR MEROPS: C14_003; -
DR GO: G0:0030693; F:caspase activity; IEA.
DR GO: G0:0008508; F:proteolysis and peptidolysis; IEA.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR InterPro: IPR002398; Peptidease_C14.
DR Pfam: PF00656; Peptidase_C14; I.
DR PRINTS: PR00376; LLIBENZYM.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.

```
Q SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;
Query Match 20.2%; Score 273; DB 6; Length 277;
Best Local Similarity 31.8%; Pred. No. 2.2e-15;
Matches 83; Conservative 34; Mismatches 100; Indels 44; Gaps 9;

Y 19 YDMSGARLALTLCVTK-----AREGEVDMEALRMFRYLKFSTWKRDPDPTAQOF 68
b 37 YKMDYPEMGLCIINNNKFNKNTGACRSGTDVDAANLRFTNLKYEVNRKNDLTR--- 93
Y 69 LEELDFEFOOTIDNWEPSVCAFV-VLMAHGEGLLKGEDEKMWLEDFEVLNNKNCKAL 127
b 94 -EILELMSVSKEDHSKRSSFICVLLSHGEGKIFGTNGP-VDLKTKLTSFRGDCRRTL 151
Y 128 RGPKPKVYIQACRGEHRDPGEELRGNELGDEELGDEGDEAVLVKNPQSIPTFTLHIY 187
b 152 TGRPKLFIQACRGTDLDCGIETDSGTE-----DDMAC-----QKIPVEADFLYAY 197
Y 188 STVEGILSYRHDKEGSGFTQTLTDV---FIHKKSILELTETFEITLMANTVMQEG--- 240
b 198 STAPGYYSWNSKDGSGWFIQSLCAALKQYVHK-----LELMHILTRVNRKVAEFESFSTD 253
Y 241 ---KPRKVNPEVOSTLRKKLY 258
b 254 STHAKQIPICVISMLTKELY 274

RESULT 11
8MKI5 PRELIMINARY; PRT; 277 AA.
C QMKI5
T 01-OCT-2002 (TremBLrel. 22, Created)
T 01-OCT-2002 (TremBLrel. 22, Last sequence update)
T 01-OCT-2003 (TremBLrel. 25, Last annotation update)
S Caspase-3.
C Canis familiaris (dog).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
X NCBI_TaxID=9615;
N [1]
P SEQUENCE FROM N.A.
LA Sano J.;
IT "canine caspase-3 gene.";
IL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
R EMBL; AB085580; BAB92962.1;
R GO; GO:0030693; F:caspace activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR002138; ICE_P10.
R InterPro; IPR001309; ICE_P20.
R InterPro; IPR002398; Peptidase_C14.
R Pfam; PF00656; Peptidase_C14; 1.
R PRINTS; PR00376; ILIBENZYM.
R SMART; SM00115; CASc; 1.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS0207; CASPASE_P10; 1.
R PROSITE; PS0208; CASPASE_P20; 1.
XN SEQUENCE 277 AA; 31334 MW; 7094C76D868DAB9 CRC64;
SQ SEQUENCE 277 AA; 31334 MW; 7094C76D868DAB9 CRC64;

Query Match 20.0%; Score 270.5; DB 6; Length 277;
Best Local Similarity 31.2%; Pred. No. 3.6e-15;
Matches 87; Conservative 40; Mismatches 99; Indels 53; Gaps 11;

Y 4 MESEMSDPQLQEEYDMSGARLALTLCVTK-----AREGEVDMEALRMFRYL 53
b 27 MDSGMS-----FDNSYKNDYPENGLCIINNNKFNKNTGACRSGTDVDAANLRFTNL 81
Y 54 KFEETMKRDPDPTAQOFLEELDFEFOOTIDNWEPSVCAFV-VLMAHGEGLLKGEDEKMWLE 112
b 82 KYEVNRKNDLTR-----EILELMSVSKEDHSKRSSFICVLLSHGEGKIFGTNGP-VDL 136
Y 113 EDLFEVLNNKNCKALRGKPKVYIIQACRGEHRDPGEELRGNELGDEELGDEGDEAVLVKN 172

137 RKVTGFFRGDYCRSLTGKPKLFIQACRGTDLDCGIETDSGIE-----DDMAC----- 184
173 NPQSIPTFTLHIYSTVEGILSYRHDKEGSGFTQTL---TDVFIHKKSILELTETFEITR 229
185 --QKIPVEADFLYAYSTAPGYYSWNSKDGSGWFIQSLCAMLKYAHK---LEFMHILTR 238
230 LMANTVMQEGPK-----RKVNPEVOSTLRKKLYL 259
239 V--NRKVATEFESFSLDSAFHGKQIPICVISMLTKELYL 275

RESULT 12
QMKI3 PRELIMINARY; PRT; 277 AA.
ID QMKI3
AC QMKI3;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Cysteine protease Cpp32.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98236830; PubMed=9575916;
RA Wang H.; Keiser J.A.;
RT "Molecular characterization of rabbit Cpp32 and its function in
vacular smooth muscle cell apoptosis.";
RL Am. J. Physiol. 274:H1132-H1140(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Wang H.; Keiser J.A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506008; AM47195.1;
DR GO; GO:0030693; F:caspace activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
XN Protease.
SQ SEQUENCE 277 AA; 31653 MW; 7BA4B12E6D43629A CRC64;

Query Match 19.7%; Score 266; DB 6; Length 277;
Best Local Similarity 29.3%; Pred. No. 8.9e-15;
Matches 81; Conservative 45; Mismatches 102; Indels 48; Gaps 10;

Y 6 SEMSDPQLQEEYDMSGARLALTLCVTK-----KAREGEVDMEALRMFRYLKF 55
b 24 SKMSDCKYLDNSYKNDYPENGLCIINNNKFNKNTGACRSGTDVDAANLRFTNLKY 83
Y 56 ESTMKRDPDPTAQOFLEELDFEFOOTIDNWEPSVCAFV-VLMAHGEGLLKGEDEKMWLE 114
b 84 EYVRNKNDLTR-----EILELMSVSKEDHSKRSSFICVLLSHGEGKIFGTNGP-IELKK 138
Y 115 LFEVLNNKNCKALRGKPKVYIIQACRGEHRDPGEELRGNELGDEELGDEGDEAVLVKNP 174
b 139 LTSFFRGDYCRSLTGKPKLFIQACRGTDLDCGIETDSGIE-----TDSGVYDVA--- 184
Y 175 QSIPTFTLHIYSTVEGILSYRHDKEGSGFTQTLTDV---FIHKKSILELTETFEITLM 231
b 185 QKIPVEADFLYAYSTAPGYYSWNSKDGSGWFIQSLCAMLKYAHK---LEFMHILTRV- 239
232 ANTEVMQEGK-----PRKVNPEVOSTLRKKLY 258
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b 240 -NRKVATEPESYSLDATFHAKKQIPCIIVSMILTKELY 274

ESULT 13
D98UI8 PRELIMINARY; PRT; 282 AA.
C Q98UI8;
T 01-JUN-2001 (T-EMBLrel. 17, Created)
T 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
T 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
E Caspase-3.
N CASP3.
S Brachydanio rerio (Zebrafish) (Danio rerio).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
C Cyprinidae; Danio.
X NCBI_TaxID=7955;
N [1]
N SEQUENCE FROM N.A.
N Yabu T., Okazaki T., Yamashita M.;
N "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
N Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
N EMBL; AB047003; BAB32409.1; -
N HSRP; P42574; 1PAU.
N MEROPS; C14.003; -
N ZFIN; ZDB-GENE-011210-1; casp3.
N GO; GO:0030693; F:caspase activity; IEA.
N GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
N InterPro; IPR002138; ICE_P10.
N InterPro; IPR001309; ICE_P20.
N InterPro; IPR002398; Peptidase_C14.
N Pfam; PF00656; Peptidase_C14; 1.
N PRINTS; PR00376; IL1BCENZYM.
N SMART; SM00115; CASC; 1.
N PROSITE; PS01122; CASPASE_CYS; 1.
N PROSITE; PS01121; CASPASE_HIS; 1.
N PROSITE; PS02027; CASPASE_P10; 1.
N PROSITE; PS02028; CASPASE_P20; 1.
N SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932E CRC64;

Query Match 19.7%; Score 266; DB 13; Length 282;
Best Local Similarity 29.2%; Pred. No. 9.1e-15;
Matches 81; Conservative 46; Mismatches 104; Indels 46; Gaps 8;
2Y 9 SDPQLQEE-----RYDMSGARLALTLCVT-----KAREGEVDMEALRMF 50
2b 22 SASQPMQVDAKQPSHAFRYSILNPNIGHCIINNNFDRITGNPNRNGTVDVAGNWNVF 81
2Y 51 RYLKPESTMKRDPTAQOFLBELDFQOTIDNWEFPVSCAFV--VLMAHGEGLLKGDEK 108
2b 82 RKLGVIVKVNQDTVAQIMQVL-----TTVAHDDHSRCASLVCLLSHGDBGVFGTDT 136
2Y 109 MYRLDLFVLNNKNCALRGKPKVYIIOACRGHRDPGELGNBELGDEBELGDEVA 168
2b 137 -VDLKSLTSLFRGDRCPSLVGPKPLFIQACRGTELPDGVETDHTD-----P 183
2Y 169 VLKNNPQIPYTDTHLYSTVEGSLYRHDKSGFTQITLDFVHKKSILELLEEIT 228
2b 184 DIPDGRKIPVEADFLYASTVPGYSWNTWTGTSWFIQSLCEM-WTKYSGSELELLQINT 242
2Y 229 RL-----MANTEVMQEGKPKRKNPEVQSTLRKKLY 258
2b 243 RVNHKVALDFESTSNMPCGDAKQIPCIIVSMILTKEMY 279

RESULT 14
Q98UI8 PRELIMINARY; PRT; 454 AA.
AC Q98UI8;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

Caspase9.
CASP9.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=20001956; PubMed=10529400;
Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
"Akt phosphorylation site found in human caspase-9 is absent in mouse
caspase-9";
Biochem. Biophys. Res. Commun. 264:550-555(1999).
EMBL; AB019600; BAA86895.1; -
PRL; JC7123; JC7123.
HSSP; P42574; 1PAU.
MEROPS; C14.010; -
MGD; MGI:1277950; Casp9.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0030693; F:caspase activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001315; CARD.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
PRINTS; PR00376; IL1BCENZYM.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASC; 1.
PROSITE; PS02029; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS02027; CASPASE_P10; 1.
PROSITE; PS02028; CASPASE_P20; 1.
SEQUENCE 454 AA; 50051 MW; 4614989AF823850F CRC64;

Query Match 19.7%; Score 266; DB 11; Length 454;
Best Local Similarity 31.0%; Pred. No. 1.7e-14;
Matches 77; Conservative 46; Mismatches 89; Indels 36; Gaps 9;
QY 36 REGSEVDMEALRMFYLKPESTMKRDPTAQOFLBELDFQOTIDNWEFPVSCAFVILMA 95
Db 218 RTGSNLDRLDKLEHFRFLRMFVVEKNDLTAKXQVATLAMEVAH---RNHRALDCFVVWIL 274
QY 96 HGEE-----GLLKGDEKAVLEDLFVLNNKNCALRGKPKVYIIOACRGHRDPGE 148
Db 275 HGCOASHLQFPAGVYGDGCVSIEKIVNFNGSGCPSLGKPKLFFIOACGGEQKHGF 334
QY 149 ELRGNEBELGDEBELGDEVAV-LKNNPQ-----SIPTVDTLHIYSTVEGSLYRHH 198
Db 335 EVACTSSQGRITLSDSEPDAPVQEGFRPLDQDAVSSLPSTPSDILVSYSTPPGFVSWRD 394
QY 199 DEKSGFIQITLDFVHKKSILE---LLEEITRLM---ANTEVMQEGKPKRKNPEVQST 252
Db 395 KXSGSWIETL-----DGILEQWARSDELQSLRLRVANA-VSEKGYKQI-PCCFNF 444
QY 253 LRKKLYLQ 260
Db 445 LRKKLFFK 452

RESULT 15
O88550 PRELIMINARY; PRT; 303 AA.
ID O88550;
AC O88550;
DT 01-NOV-1998 (T-REMBLrel. 08, Created)
DT 01-NOV-1998 (T-REMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (T-REMBLrel. 25, Last annotation update)
DE Caspase-7.
OS Rattus norvegicus (Rat).

Mon Mar 22 14:13:35 2004

1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
2 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
3 NCBI_TaxID=10116;
4 [1]
5 SEQUENCE FROM N.A.
6 TISSUE=Spleen;
7 Forghani F., Roy S.;
8 "Rat caspase-7 sequence."
9 Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
10 EMBL; AF072124; AAC24011.1; -.
11 HSSP; P42574; IPAU.
12 MEROPS; C14.004; -.
13 GO; GO:0030693; P:caspase activity; IEA.
14 GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
15 InterPro; IPR002138; ICE_P10.
16 InterPro; IPR001309; ICE_P20.
17 InterPro; IPR002398; Peptidase_C14.
18 Pfam; PF00656; Peptidase_C14; 1.
19 PRINTS; PR00376; ILIHCENZYME.
20 SMART; SM00115; CASC; 1.
21 PROSITE; PS01122; CASPASE_CYS; 1.
22 PROSITE; PS01121; CASPASE_HIS; 1.
23 PROSITE; PS0207; CASPASE_P10; 1.
24 PROSITE; PS0208; CASPASE_P20; 1.
25 SEQUENCE 303 AA; 34324 MW; A71728754BF199DD CRC64;

Query Match 19.6%; Score 264.5; DB 11; Length 303;
Best Local Similarity 34.2%; Pred. No. 1.4e-14;
Matches 79; Conservative 35; Mismatches 92; Indels 25; Gaps 8;
Y 36 REGSEVDMEALERMYLYKFEETMKEDPTAQQLFELDEFOQTIDNWEPPVSCAFVVLMA 95
b 87 RRGTDKDAEALFKCFSLGFEVTVINDSCAKM---QDLRRASEEDHSNACFACVLLS 143
Y 96 HGEDEGLKGEDEKMAVLEDLFEVLNNKNCALRGPKVYIIQACRGEHRDPGEELRGNEE 155
b 144 HGEENLIYKGD-GVTPFKOLTAHFRGDRCKTLLEKPKLFFIQACRGTELDG----- 194
Y 156 LGODELGGDEVAVLKNPQ-SIPYTDTHLYSTVEGVLVYRHDKSGFGIQLTLDVFI 214
b 195 IQADSGPINDTDA-----NPKYKIPVEADFLFAYSTVPGYISWRNPGKSWFQALCSI-L 249
Y 215 HKKGSILELTEITRL---MANTVMEQCKPR-----KVNPEVQSTLRKLY 258
b 250 NEHGKDLINQILITRVNDRVARHFESQSDPRFNEKKQIPCMVSLTKELY 300

earch completed: March 19, 2004, 11:24:11
ob time : 39.2908 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

run on: March 19, 2004, 11:09:05 ; Search time 10.3586 Seconds
(without alignments)
1306.961 Million cell updates/sec

title: US-09-989-903-2
effect score: 1350
sequence: 1 KPDMESEMSDPOQLQERYD.....KPRKVNPEVQSTLRKLYLQ 260

icoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1332	98.7	257	1	ICEE MOUSE
2	940.5	69.7	242	1	ICEE HUMAN
3	290.5	21.5	424	1	ICE2 CHICK
4	276.5	20.5	435	1	ICE2 MOUSE
5	276	20.4	277	1	ICE3 MOUSE
6	274.5	20.3	435	1	ICE2 HUMAN
7	274	20.3	277	1	ICE3 RAT
8	273	20.2	277	1	ICE3 HUMAN
9	263	19.5	277	1	ICE3 CRILLO
10	259.5	19.2	496	1	CEB3 CAEVU
11	257	19.0	416	1	ICE9 HUMAN
12	255.5	18.9	303	1	ICE7 HUMAN
13	254.5	18.9	303	1	ICE7 MOUSE
14	253	18.7	503	1	CEB3 CAREL
15	249.5	18.5	303	1	ICE7 MESAU
16	249.5	18.5	382	1	ICEB XENLA
17	243	18.0	339	1	ICE DROME
18	242	17.9	480	1	ICE8 MOUSE
19	240.5	17.8	293	1	ICE6 HUMAN
20	235	17.4	276	1	ICE6 MOUSE
21	231.5	17.1	282	1	ICE3 XENLA
22	227.5	16.9	323	1	ICE1 DROME
23	226.5	16.8	299	1	ICE8 HUMAN
24	220	16.3	479	1	ICE2 RAT
25	219	16.2	312	1	ICE2 RAT
26	217.5	16.1	386	1	ICEA XENLA
27	215.5	16.0	404	1	IIBC HUMAN
28	213	15.8	410	1	IIBC FELCA
29	211	15.6	404	1	IIBC CANFA
30	205	15.2	402	1	IIBC RAT
31	203	15.0	418	1	ICE5 HUMAN
32	201.5	14.9	402	1	IIBC MOUSE
33	200.5	14.9	405	1	IIBC HORSE

34	198.5	14.7	404	1	IIBC PIG
35	198	14.7	521	1	ICEA HUMAN
36	196.5	14.6	419	1	ICEC MOUSE
37	190.5	14.1	377	1	ICE4 HUMAN
38	188.5	14.0	373	1	ICE4 MOUSE
39	175	13.0	377	1	ICED BOVIN
40	112	8.3	484	1	CFLA MOUSE
41	102	7.6	1429	1	NOS1 RAT
42	101.5	7.5	480	1	CFLA HUMAN
43	99	7.3	505	1	ATPA CALSU
44	95.5	7.1	843	1	MVPA DICDI
45	95.5	7.1	880	1	RA50 PYRAB

RESULT 1
ICEE MOUSE
ID ICEE MOUSE STANDARD; PRT; 257 AA.
AC O89094;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (Mini-ICE) (MICE).
GN CASP14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=C57BL/6J;
RA MEDLINE=99040667; PubMed=9823333;
RA Ahmad M., Srinivasula S.M., Hegde R., Mukattash R.,
RA Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification and characterization of murine caspase-14, a new
RT member of the caspase family";
RL Cancer Res. 58:5201-5205(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryo;
RA MEDLINE=99222069; PubMed=10203698;
RA Van de Craen M., Van Loo G., Pyde S., Van Criekeinge W.,
RA Van den brande I., Molemans F., Fiers W., Declercq W.,
RA Vandenabeele P.;
RT "Identification of a new caspase homologue: caspase-14";
RL Cell Death Differ. 5:838-846(1998).
RN [3]
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.
RC MEDLINE=99009076; PubMed=9792675;
RA Hu S., Snipas S.J., Vincenz C., Salvesen G., Dixit V.M.;
RT "Caspase-14 is a novel developmentally regulated protease";
RL J. Biol. Chem. 273:29648-29653(1998).
CC -!- FUNCTION: Seems to be involved in the death receptor and granzyme
CC B apoptotic pathways. May function as a downstream signal
CC transducer of cell death. May play a role in ontogenesis and skin
CC physiology.
CC -!- SUBUNIT: May dimerize with large prodomain caspases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
CC -!- TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain
CC and kidney.
CC -!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

EMBL; AF092997; AAC63364.1; -
EMBL; AJ007750; CAA07678.1; -
EMBL; P29466; 1ICE.
MEROPS; C14.018; -
MGD; MGI:1335092; Casp14.
GO; GO:0006917; P:induction of apoptosis; IDA.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
InterPro; IPR002398; Peptidase C14.
Pfam; PF00656; Peptidase C14; 1.
PRINTS; PR001376; IL1BCENZME.
SMART; SM00115; CASG; 1.
PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Apoptosis; Zymogen.
PROPEP 1 7
CHAIN 8 ?
ACT SITE 93 93
ACT SITE 136 136
MUTAGEN 136 136
SEQUENCE 257 AA; 29458 MW; A228D8DFBAEB84 CRC64;
Query Match 98.7%; Score 1332; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-93;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4 MESEMSDPOPLQEEYDMSGARLALTCVTKAREGSEVDMALERMFRYLKFKSTMKRDP 63
1 MESEMSDPOPLQEEYDMSGARLALTCVTKAREGSEVDMALERMFRYLKFKSTMKRDP 60
64 TAAQFLBELDFQOITDNEEVPSCAFVVLMAHGEGLKGEDEKMWLEDFEVLNKN 123
61 TAAQFLBELDFQOITDNEEVPSCAFVVLMAHGEGLKGEDEKMWLEDFEVLNKN 120
124 CKAALRKPKVYIIQACRGHRDPGSELRNGLGDEGLGDEVAVLKNNPQSIPTTDT 183
121 CKAALRKPKVYIIQACRGHRDPGSELRNGLGDEGLGDEVAVLKNNPQSIPTTDT 180
184 LHYSTVEGVLVSRHDEKSGFIQTLTVFHKHGSILELFEETRLMANTENVQEGKPR 243
181 LHYSTVEGVLVSRHDEKSGFIQTLTVFHKHGSILELFEETRLMANTENVQEGKPR 240
244 KVNPEVQSTLRKLYLQ 260
241 KVNPEVQSTLRKLYLQ 257

RESULT 2
CEE HUMAN STANDARD; PRT; 242 AA.
D_ICEE HUMAN
C P31944; O95823;
T 01-JUL-1993 (Rel. 26, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 15-MAR-2004 (Rel. 43, Last annotation update)
E Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
N CASP14.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_Taxid=9606;
[1]
P SEQUENCE FROM N.A.
C TISSUE=Brain;
X MEDLINE=22168928; PubMed=12181750;
A Pistrutto G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L.,
Xari C., Lazebnik Y., Rodeck U., Alnemri E.S.;

"Expression and transcriptional regulation of caspase-14 in simple
and complex epithelia";
Cell Death Differ. 9:995-1006(2002).
[2]
SEQUENCE OF 68-74; 137-147 AND 154-162.
TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
Vandekerckhove J.;
"Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes";
Electrophoresis 13:960-969(1992).
CC FUNCTION: May be involved in the death receptor and granzyme B
apoptotic pathways. May function as a downstream signal transducer
of cell death.
CC SUBUNIT: May dimerize with large prodomain caspases.
CC SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC SIMILARITY: Belongs to peptidase family C14.
CC
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or send an email to license@isb-sib.ch).
CC
EMBL; AF097874; AAD16173.1; -
PIR; JC7517; JC7517.
HSSP; P29466; 1ICE.
Aarhus/Ghent-2DPAGE; 6109; IEF.
MEROPS; C14.018; -
Genew; HGNC:1502; CASP14.
MIM; 605848; -
GO; GO:0004199; F:caspase activity; TAS.
GO; GO:0008544; P:epidermal differentiation; TAS.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
InterPro; IPR002398; Peptidase C14.
Pfam; PF00656; Peptidase C14; 1.
PRINTS; PR00376; IL1BCENZME.
SMART; SM00115; CASG; 1.
PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Apoptosis; Zymogen.
PROPEP 1 7
CHAIN 8 ?
ACT SITE 93 93
ACT SITE 132 132
BY SIMILARITY.
SEQUENCE 242 AA; 27679 MW; E539FB7B8DD808A2 CRC64;
Query Match 69.7%; Score 940.5; DB 1; Length 242;
Best Local Similarity 71.3%; Pred. No. 3.7e-64;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;
8 MSDPQLOEERYDMSGARLALTCVTKAREGSEVDMALERMFRYLKFKSTMKRDP 67
1 MSNPSLEEKYDMSGARLALTCVTKAREGSEEDLDALHMFRLQAFESTMKRDP 60
68 FLELDFEFOOTIDNWEVPSCAFVVLMAHGEGLKGEDEKMWLEDFEVLNKNCKAL 127
61 FQELEKFTQQAIDRSDFVSCAFVVLMAHGEGLKGEDEKMWLEDFEVLNKNCKAL 120
128 RQKPKVYIIQACRGHRDPGSELRNGLGDEGLGDEVAVLKNNPQSIPTTDTLHI 186
121 RQKPKVYIIQACRGHRDPGSELRNGLGDEGLGDEVAVLKNNPQSIPTTDTLHV 168
187 YSTVEGVLVSRHDEKSGFIQTLTVFHKHGSILELFEETRLMANTENVQEGKPR 246
169 YSTVEGVLVSRHDEKSGFIQTLTVFHKHGSILELFEETRLMANTENVQEGKPR 228

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247 PVQSTLRKLYLQ 260
||:|||||:|
229 PRIQSTLRKLYLQ 242

RESULT 3
CASP2-2 SUBUNIT P12 (BY SIMILARITY).
CARD.
BY SIMILARITY.
BY SIMILARITY.
Missing (in isoform ICH-1S).
/FTID=VSP_000803.
DETDRGVQDQKAMRNTKRGSTYIEALTVFAEDSDTHVA
MICGYACLGTAAMRNTKRGSTYIEALTVFAEDSDTHVA
DMLVKNRQIKQREGVAPGTEFHRCCKEMSEYCSLCLRDLYL
PGYVPGK -> GVGSIHLPLPCCHCICCSMROTGEWI
REMAKNGQIPQAVRVVMTQTKKISSVCVCLHAPI (in
isoform ICH-1S).
/FTID=VSP_000804.
792810508B8B2F60 CRC64;
SQ SEQUENCE 424 AA; 47959 MW; 792810508B8B2F60 CRC64;

Query Match 21.5%; Score 290.5; DB 1; Length 424;
Best Local Similarity 31.0%; Pred. No. 9.3e-15;
Matches 72; Conservative 53; Mismatches 94; Indels 13; Gaps 5;

QY 36 REGSEVDMEALRMFVYKLFSTMKRDPFTAQQLLELDEFQQTIDNWEPEVSCAFVVLMA 95
DQ 190 RSGGDVDCASLELLFKHLYQVTVFHDQSAEEMESALERSKLPDH--QDVDSICVALLS 247
QY 96 HGEGLLKGDEKVRLEDLPEVLNNKNCALRGKPKVYIIQACRGSHRDPGBELRGNEE 155
DQ 248 HGVGEGVGTGKLLQQLQEAFLFDNANCPNLQNKPMPTIACRGDETDGVDQDQKE 307
QY 156 LG--GDEELGGDEVAVLKNNPQSIPTVTLHTYSTVEGVLSTYRHDKSGSGFIQITLV 212
DQ 308 RSDSPGCESDANKEENLK--LRLPTRSDMICGYACLGTAAMRNTKRGSTYIEALTV 364
QY 213 FTH--KKSILELFEITRLMANTENVQEGKP---RKVNPEVQSTLRKLYL 259
DQ 365 PAEDSRDTHVADMLVKNRQIKQREGVAPGTEFHRCCKEMSEYCSLCLRDLYL 416

RESULT 4
ICE2 MOUSE
ID ICE2 MOUSE STANDARD; PRT; 435 AA.
AC R29594; O08737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2
protein).
DE CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=95047319; PubMed=7958843;
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
protein similar to the product of the Caenorhabditis elegans cell
death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
RL Genes Dev. 8:1613-1626(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaabeele P., Declercq W., van den Brande I.,
RA van Loo G., Molemans F., Schotte P., van Criekeinge W., Bayaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92328780; PubMed=1378265;
RA Kumar S., Tomooka Y., Noda M.;
```

I Identification of a set of genes with developmentally down-regulated expression in the mouse brain.";
L Biochem. Biophys. Res. Commun. 185:1155-1161(1992).

-I- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Might function by either activating some proteins required for cell death or inactivating proteins necessary for cell survival. May be important in multistep carcinogenesis.

-I- SUBUNIT: Heterodimer of a small and a large subunit (By similarity).

-I- TISSUE SPECIFICITY: High level expression seen in the embryonic CNS, liver, lung, kidney, small intestine, and hair follicles of vibrissae. Moderate expression seen in the skin, oral mucosa, skeletal muscle, submandibular gland and thymus. In the adult, it is highly expressed in spleen, lung and kidney. Moderately in the brain, heart, testis, liver. Low levels in the thymus, skeletal muscle, ovary and gut.

-I- DEVELOPMENTAL STAGE: During embryonic development is highly expressed in several types of mouse tissue undergoing high rates of programmed cell death such as central nervous system and kidney.

-I- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT THAT OF OTHER CASPASES (BY SIMILARITY).

-I- SIMILARITY: Belongs to peptidase family C14.

-I- SIMILARITY: Contains 1 CARD domain.

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R EMBL: D28492; BAA25876.1; ALT INIT.
R EMBL: Y13085; CAA73527.1; ALT_INIT.
R HSSP: P42574; ICP3.

R MEROPS: C14.006; --.
R MGD: MGI:97295; Casp2.

R InterPro: IPR001315; CARD.

R InterPro: IPR002138; ICE_P10.

R InterPro: IPR001309; ICE_P20.

R InterPro: IPR002398; Peptidase_C14.

R Pfam: PF00619; CARD; 1.

R Pfam: PF00656; Peptidase_C14; 1.

R PRINTS: PR00376; ILIBCEZYME.

R SMART: SM00114; CARD; 1.

R SMART: SM00115; CAS; 1.

R PROSITE: PS02029; CARD; 1.

R PROSITE: PS01122; CASPASE_CYS; 1.

R PROSITE: PS01121; CASPASE_HIS; 1.

R PROSITE: PS02027; CASPASE_P10; 1.

R PROSITE: PS02028; CASPASE_P20; 1.

R Hydroxylase; Thiol protease; Apoptosis; Zymogen.

R PROPEP 1 152 BY SIMILARITY.

R CHAIN 153 316 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).

R CHAIN 317 435 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).

R CHAIN 331 435 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).

R DOMAIN 15 103 CARD.

R ACT_SITE 260 260 BY SIMILARITY.

R ACT_SITE 303 303 BY SIMILARITY.

R MUTAGEN 303 303 C-XG: LOSS OF FUNCTION.

R CONFLICT 71 71 MISSING (IN REF. 1).

R SEQUENCE 435 AA; 48986 MW; 8984E6AA76E7A676 CRC64;

Query Match 20.58; Score 276.5; DB 1; Length 435;

Best Local Similarity 30.68; Pred. No. 1.1e-13;

Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

36 REGSEVDEALERMFYKPESTMKRQDPTAQOFLDEFTQIDNWEPEVSCAFVILWA 95

202 RSGGDVHTTLVTFLKLLGVNVHLVDQTAQOEKQLNQFAQ-LPAHRVTDSCV-VALLS 259

QY 96 HGEGLLKGEDEKMWLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPG---EELRG 152
DB 260 HGVGGYGVGDQKLQEQEVRFLFDNANCSLQNKPMFPIQACRDETDGRVDQDQGN 319
QY 153 NEELGGDEELGDEAVLKNPNQSIPTDTLHISTVGYLSYRHDKSGSFIOFLTV 212
DB 320 HTQPGCEESDAGKEELMK---NRLPTRSDMICGYACLGKNAAMRNTRKGSWYIEALTQV 376
QY 213 FIHKKS---LLELTETETRLWANTVWQEGKP---RKVNPEVQSTLRKLYL 259
DB 377 FSRACDMHVADMLVKVNLIKEREGYAPGTETFRCKEMSEYCTLCQQLYL 428

RESULT 5

ICE3 MOUSE STANDARD; PRT; 277 AA.
AC 070677; O08668; Q9QW14;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE).
DE CASP3 OR CPP32.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224429; PubMed=9070890;
RA Mukasa T., Urace K., Momoi M.Y., Kimura I., Momoi T.;
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
RT activation of CPP32 in the apoptosis induced by a withdrawal of
RT NGF.";
RL Biochem. Biophys. Res. Commun. 231:770-774(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Loo G., Molemans F., Schotte P., van Criekeinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler C.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
A Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length
T human and mouse cDNA sequences";
L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
N [6]
P SEQUENCE OF 58-277 FROM N.A.
A Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
A Fortin J.-P., Sekaly R.-P.;
T "Multiple pathways of apoptosis converging on the CPP32 protease.";
L Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
C C -1- FUNCTION: Involved in the activation cascade of caspases
C responsible for apoptosis execution. At the onset of apoptosis it
C proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
C 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
C element binding proteins (SREBPs) between the basic helix-loop-
C helix leucine zipper domain and the membrane attachment domain.
C Cleaves and activates caspase-6, -7 and -9 (By similarity).
C Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
C cytokine which is involved in a variety of inflammatory processes.
C C -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
C (by similarity).
C C -1- SUBCELLULAR LOCATION: Cytoplasmic.
C C -1- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
C kidney and heart. Lower expression in brain, skeletal muscle and
C testis.
C C -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
C TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
C LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
C PROPEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
C CASPASE-7 PROPEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
C VICE VERSA (BY SIMILARITY).
C C -1- SIMILARITY: Belongs to peptidase family C14.
C
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C or send an email to license@isb-sib.ch).
C
C EMBL; U54803; AAC52768.1; -;
C EMBL; U54802; AAC52768.1; JOINED.
C EMBL; U49929; AAC52764.1; -;
C EMBL; D86352; BAA21727.1; -;
C EMBL; Y13086; CAA73528.1; -;
C EMBL; U19522; AAC53196.1; -;
C EMBL; BC038825; AAH38825.2; -;
C EMBL; U63720; AAD09504.1; -;
C F1R; JC5410; JCS410.
C HSP; P42574; IPAU.
C MEROPS; C14.003; -;
C MGD; MGI:107739; Casp3.
C InterPro; IPR002138; ICE_p10.
C InterPro; IPR001309; ICE_p20.
C InterPro; IPR002398; Peptidase_C14.
C Pfam; PF00656; Peptidase_C14; 1.
C PRINTS; PR00376; ILIBENZYM.EMBL.
C SMART; SMO0115; CASc; 1.
C PROSITE; PS01122; CASPASE_CYS; 1.
C PROSITE; PS01121; CASPASE_HIS; 1.
C PROSITE; PS02027; CASPASE_P10; 1.
C PROSITE; PS02029; CASPASE_P20; 1.
C W Hydroxylase; Thiol protease; Zymogen; Apoptosis.
T PROPEP 1 9 BY SIMILARITY.
T PROPEP 10 28 BY SIMILARITY.
T CHAIN 29 175 APOPAIN P17 SUBUNIT.

FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT SITE 121 121 BY SIMILARITY.
FT ACT SITE 163 163 BY SIMILARITY.
FT CONFLICT 17 17 E -> G (IN REF. 2).
FT CONFLICT 51 51 N -> T (IN REF. 2).
FT CONFLICT 63 65 SRS -> ARN (IN REF. 6).
FT CONFLICT 84 84 Q -> E (IN REF. 2).
FT CONFLICT 95 95 D -> E (IN REF. 2).
FT CONFLICT 97 97 L -> M (IN REF. 2).
FT CONFLICT 128 128 Y -> F (IN REF. 2).
FT CONFLICT 135 135 E -> D (IN REF. 2).
FT CONFLICT 231 231 E -> Q (IN REF. 6).
FT CONFLICT 262 262 I -> F (IN REF. 6).
SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;
Query Match 20.4%; Score 276; DB 1; Length 277;
Best Local Similarity 33.3%; Pred. No. 6.7e-14;
Matches 79; Conservative 39; Mismatches 81; Indels 38; Gaps 9;
OY 35 AREGSEVDMEALERNFRVLYKFEKSTWKRDPDPTAQQLLELDFEQQTIDNWEFVSCAFV-VL 93
DB 63 SRSGTDVDAANLRFTFMGLKYQVRNKNDLTREDILELMD-----SVSKEDHSKSSFCVCI 118
OY 94 MAHGEGILLKGDDEKQVLEDLFEVLNNKNCALRGPKKVYIIQACRGEHRDPGEELRGN 153
DB 119 LSHGDEGIYGTNGP-VELKKLTSTFRGDCYCSLTGKPKLFIQACRGTLEDGIE----- 173
OY 154 BELGDEELGGDEVAVLKNPQSTPTVYDTLHIVSTVEGYLSYRPHDEKSGGFTOTLTD-- 211
DB 174 TDSGTDEENA-----CQKIPVEADFLYASTAGPYYSWRNSKDGSWFIQSLCSML 223
OY 212 -VPIHKSGSILELITEITRLMANTVMEQK-----PRKVNPEVQSTLRKKLY 258
DB 224 KUYANK-----LEFMILTRV--NRKVATEFESFLDSTFFHAKQIPICIVSMILTLEY 274
RESULT 6
ICE2 HUMAN STANDARD; PRT; 435 AA.
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
DE 11/18).
GN CASP2 OR ICH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Fetal brain;
RX MEDLINE=94373811; PubMed=8087842;
RA Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;
RT "Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
RT regulators of programmed cell death.";
RL Cell 78:739-750 (1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ALA-161 AND
RP GLY-424.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.B., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Deebber A., Martinka S., Maupin R.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP CLEAVAGE SITES.
RX MEDLINE=96206041; PubMed=8654923;
RA Xue D., Shahan S., Horvitz H.R.;

[4] SEQUENCE FROM N.A., AND VARIANT GLU-190.
P Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
A Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
A Schackwitz W.S., Sherwood J.K., Witak L.A., Nickerson D.A.;
L Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
N [5]
P SEQUENCE FROM N.A., AND VARIANT GLU-190.
C TISSUE=Lymph;
X MEDLINE=22388257; PubMed=12477932;
C Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Tothyluk S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Rahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.B.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length
T human and mouse cDNA sequences";
L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
N [6]
P SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
X MEDLINE=95319529; PubMed=7596430;
C Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,
A Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,
A Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,
A Miller D.K.;
T "Identification and inhibition of the ICE/CED-3 protease necessary
T for mammalian apoptosis";
L Nature 376:37-43(1995).
N [7]
P X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
X MEDLINE=96266352; PubMed=8673606;
C Retonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
A Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
A Thornberry N.A., Becker J.W.;
T "The three-dimensional structure of apopain/CPP32, a key mediator of
T apoptosis";
L Nat. Struct. Biol. 3:619-625(1996).
N [8]
P X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
X MEDLINE=97197830; PubMed=9045680;
C Mittl P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
A Priestle J.P., Tomaselli K.J., Gruetter M.G.;
T "Structure of recombinant human CPP32 in complex with the
T tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone";
L J. Biol. Chem. 272:6539-6547(1997).
N [9]
P X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
X MEDLINE=96353838; PubMed=8755496;
C Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
A Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
A Levy M.A., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
A Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDewitt P.J.,
A Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
A Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
T "Potent and selective nonpeptide inhibitors of caspases 3 and 7
T inhibit apoptosis and maintain cell functionality";
L J. Biol. Chem. 275:16007-16014(2000).
N [10]
P PROCESSING.
X MEDLINE=96353838; PubMed=8755496;
C Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
A Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
A Litwack G., Alnemri E.S.;
T "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
T apoptotic cysteine protease containing two FADD-like domains";
L Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
N [11]
P CLEAVAGE OF HUNTINGTIN.
X MEDLINE=96331285; PubMed=8696339;
C Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
A Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
A Vaillancourt J.P., Hayden M.R.;
T "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
T is modulated by the polyglutamine tract";
L Nat. Genet. 13:442-449(1996).
C -!- FUNCTION: Involved in the activation cascade of caspases
C responsible for apoptosis execution. At the onset of apoptosis it
C proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
C 216-Asp-1-Gly-217 bond. Cleaves and activates sterol regulatory
C element binding proteins (SREBPs) between the basic helix-loop-
C helix leucine zipper domain and the membrane attachment domain.
C Cleaves and activates caspase-6, -7 and -9. Involved in the
C cleavage of huntingtin.
C -!- ENZYME REGULATION: Inhibited by isatin sulfonamides.
C -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
C -!- SUBCELLULAR LOCATION: Cytoplasmic.
C -!- TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
C and kidney. Moderate levels in brain and skeletal muscle, and low
C in testis. Also found in many cell lines, highest expression in
C cells of the immune system.
C -!- PTM: CLEAVAGE BY GRANTZYME B, APAF-1, CASPASE-6, -8 AND -10
C GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
C PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
C ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
C OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
C AND VICE VERSA.
C -!- SIMILARITY: Belongs to peptidase family C14.
C
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C the European Bioinformatics Institute. There are no restrictions on its
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C or send an email to license@isb-sib.ch).
C
C -----
C EMBL: U13737; AA65015.1; -
C EMBL: U13738; AA60355.1; -
C EMBL: U26943; AAA7429.1; -
C EMBL: AJ413269; CAC89866.1; -
C EMBL: AY219866; AAO25654.1; -
C EMBL: BC016926; AAH16926.1; -
C EMBL: PIR; A55315; A55315.
C PDB: 1PAU; 07-JUL-97.
C PDB: 1CP3; 24-DEC-97.
C PDB: 1GFV; 23-JUN-00.
C MEROPS: C14.003; -
C Genew: HGNC:1504; CASP3.
C MIM: 600636; -
C GO: GO:004208; P:caspase-3 activity; TAS.
C GO: GO:008624; P:induction of apoptosis by extracellular sig. .; TAS.
C GO: GO:008629; P:induction of apoptosis by intracellular sig. .; TAS.
C GO: GO:009405; P:apoptosis; TAS.
C InterPro: IPR002138; ICE p10.
C InterPro: IPR001309; ICE p20.
C InterPro: IPR002398; Peptidase C14.
C Pfam: PF00656; Peptidase C14; 1.
C PRINTS: PR00376; ILBENZYM.
C SMART: SM00115; CASC.1
C PROSITE: PS01122; CASPASE_CYS; 1.
C PROSITE: PS01121; CASPASE_HIS; 1.
C PROSITE: PS0207; CASPASE_P10; 1.
C PROSITE: PS0208; CASPASE_P20; 1.
C Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
KW

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W 3D-structure. 1 9
T PROPEP 10 28
T CHAIN 29 175
T CHAIN 176 277
T ACT_SITE 121 121
T ACT_SITE 163 163
T VARIANT 190 190
T CONFLICT 31 36
T STRAND 36 36
T STRAND 43 51
T HELIX 57 59
T TURN 60 60
T TURN 65 66
T HELIX 67 80
T TURN 81 82

Query Match 20.2%; Score 273; DB 1; Length 277;
Best Local Similarity 31.5%; Pred. No. 1.1e-13;
Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;

Y 6 SEMSDPQLOEEDYDMSGARLATLTCVTK-----AREGSEVDMEALERMERYLK 55
b 24 SEMSDGISLDSNYSKMDYPMGLCIINNNKFNHKTGTSRGTDVDAANLRETFNLYK 83
Y 56 ESTMKRDPTAQQLFLEELDEPQQTIDNWEFPVSCAFV-VLMARGEGLLKGDEKVRLED 114
b 84 EVRNKNDLTR-----EIVELMRDVSXEDHSKRSSFVCLLSHGEEGIPTNGP-VDLKK 138
Y 115 LFEVLNNKCKALRGPKVYIIACGEHRDCEELRGNEELGGDEELGDEAVLKNKP 174
b 139 ITNFRGDRCRSLTGPKLFIIOACRGTELDGIE-----TDSGVD-----DMACHK--- 186
Y 175 QSIPTVYDTLHIXSTVEGYLSYRHDKSGSGFIQTLTDVFIHKKGSILETETRLMANT 234
b 187 --IPVDADFLIYASTAGPYYSWNSKSGSWFIQSLC-AMLKQYADKLRFHMLTRV--NR 241
Y 235 EVMQEGK-----PRKNPEVQSTLRKKLY 258
b 242 KVATEFESFSFDATFFHAKQIQCIVSMLTKELY 274

RESULT 9
ID ICE3_CRIL0 STANDARD; PRT; 277 AA.
AC Q60431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1).
EN CASP3 OR CPP32.
DS Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
DC Cricetus.
DC NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96183185; PubMed=8605970;
RA Wang X., Zelenski N.G., Yang J., Sakai J., Brown M.S.,
RA Goldstein J.L.;
RT CPP32 cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis";
RL EMBO J. 15:1012-1020(1996).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-

```


[9] SEQUENCE FROM N.A. (ISOFORM 1).
P Thomas D.,
L Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
N [10]
P SEQUENCE FROM N.A. (ISOFORM 1).
C TISSUE=Eye, and Lymph;
X MEDLINE=22388257; PubMed=12477932;
A Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
A Brownstein M.J., Ustin T.B., Tohilyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
UT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
C -!- FUNCTION: Involved in the activation cascade of caspases
C responsible for apoptosis execution. Binding of caspase-9 to Apaf-
C 1 leads to activation of the protease which then cleaves and
C activates caspase-3. Proteolytically cleaves poly(ADP-ribose)
C polymerase (PARP).
C -!- FUNCTION: Isoform 2 lacks activity is an dominant-negative
C inhibitor of caspase-9.
C -!- SUBUNIT: Heterodimer of a 35 kDa (P35) and a 10 kDa (P10) subunit.
C Caspase-9 and APAF1 bind to each other via their respective NH2-
C terminal CEP-3 homologous domains in the presence of cytochrome C
C and ATP. Interacts with BIRC7.
C -!- ALTERNATIVE PRODUCTS:
C Event=Alternative splicing; Named isoforms=2;
C Name=1; Synonyms=9L, Alpha; displayed;
C IsoId=P5511-1; Sequence=displayed;
C Name=2; Synonyms=9S, Beta;
C IsoId=P5511-2; Sequence=VSP_000818;
C -!- TISSUE SPECIFICITY: Ubiquitous, with highest expression in the
C heart, moderate expression in liver, skeletal muscle, and
C pancreas. Low levels in all other tissues.
C -!- PTM: CLEAVAGES AT ASP-315 BY GRANZYME B AND AT ASP-330 BY CPP32
C GENERATE THE TWO ACTIVE SUBUNITS. CASPASE-8 AND -10 CAN ALSO BE
C INVOLVED IN THESE PROCESSING EVENTS.
C -!- SIMILARITY: Belongs to peptidase family C14.
C -!- SIMILARITY: Contains 1 CARD domain.
C This SWISS-PROT entry is copyright. It is produced through a collaboration
C between the Swiss Institute of Bioinformatics and the EMBL outstation -
C the European Bioinformatics Institute. There are no restrictions on its
C use by non-profit institutions as long as its content is in no way
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C entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
C or send an email to license@isb-sib.ch).
C
C EMBL; U56390; AAC50640.1; -;
C EMBL; U60521; AAC50776.1; -;
C EMBL; AB019205; BAA82697.1; -;
C EMBL; AB019137; BAA82697.1; JOINED.
C EMBL; AB019198; BAA82697.1; JOINED.
C EMBL; AB019199; BAA82697.1; JOINED.
C EMBL; AB019200; BAA82697.1; JOINED.
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C EMBL; AB019204; BAA82697.1; JOINED.
C EMBL; AB019205; BAA82697.1; JOINED.

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DR EMBL; AB015653; BAA78780.1; -;
DR EMBL; AB020979; BAA87905.1; -;
DR EMBL; AF110376; AAD13615.1; -;
DR EMBL; AL512883; CAC42423.1; -;
DR EMBL; AY214168; AAO21133.1; -;
DR EMBL; BC002452; AAO2452.1; -;
DR EMBL; BC006463; AAO06463.1; -;
DR PDB; 3YGS; 19-APR-00.
DR MEROPS; C14.010; -;
DR Genew; HGNC:1511; CASP9.
DR MIM; 602234; -;
DR GO; GO:0004211; F.caspase-9 activity; TAS.
DR GO; GO:0004197; F.cysteine-type endopeptidase activity; TAS.
DR GO; GO:0008047; F.enzyme activator activity; TAS.
DR GO; GO:0008233; F.peptidase activity; TAS.
DR GO; GO:0008632; P.apoptotic program; TAS.
DR GO; GO:0008635; P.caspase activation via cytochrome c; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
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DR PROSITE; PS0209; CARD; 1.
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DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW Polymorphism; 3D-structure.
FT PROPEP 1 ? POTENTIAL.
FT CHAIN ? 315 CASPASE-9 SUBUNIT P35.
FT PROPEP 316 330 CASPASE-9 SUBUNIT P10.
FT CHAIN 331 416 CARD.
FT DOMAIN 1 92 CARD.
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FT ACT_SITE 287 287 Missing (in isoform 2).
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FT VARIANT 114 114 /FTId=VAR_015418.
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DB 178 RTRTGSNIDCEKLRFRFSLHFVMEYKGLTAKKMWLALLELAQPDHG---ALDCCVVI 234
QY 94 MANGEE-----GLLKGEDEKMKVRLEDLFVNLNKNCKALKSKPKVYIIQACRGEHRDP 146
DB 235 LSHGQCASHLQFFGAVYGTDCGVPSEKIVNFNGTSCPSLGGKPKLFIQACGEQKH 294
QY 147 GBEALRGNEELGGDEELGGDEAVLKNPQ-----SITYTDTLHI 186
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R InterPro; IPR002398; Peptidase C14.
R Pfam; PF00656; Peptidase C14; 1.
R PRINTS; PRO0376; ILIBENZYME.
R SMART; SMO0115; CASC; 1.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS02027; CASPASE_P10; 1.
R PROSITE; PS02028; CASPASE_P20; 1.
W Hydroxylase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
W 3D-structure.
T PROPEP 1 23
T CHAIN 24 198
T PROPEP 199 206
T CHAIN 207 303
T ACT_SITE 144 144
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HFSQSDPHFHEKQIPCVSNLTKELYSQ -> MESCS
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MLILDRSQMLTSSPPIPRFQAITRGGAQEEAPGLCKPSA
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MUTAGEN 186 186
C-A: NO APOPTOTIC ACTIVITY.
D -> E (IN REF. 5).
CONFLICT 194 194
G -> A (IN REF. 1).
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Best Local Similarity 30.5%; Pred. No. 2.7e-12;
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Y 18 RYDMSGARLALTCVTK-----ARGSEVDMEALERFRYKPESTWKRPDPA-- 65
b 59 QYNNPFKGLKCIINNKNFVKVTGMVGRNGTDKDAEALFKFRSGFVIVYVDCSAK 118
Y 66 -QQPLELDELFOQTIDNWEFPVSCAFVLMAGEGLLKGDEKVMVRLDLPVLNNKNC 124
b 119 MQDLLKXASEDHT-----NAACFACILLSHGENVVYGKD-GVTPIKDLTAHPRGDR 171
Y 125 KALRGKPKVYIIOACRGEHDPGEELRGNEELGDEELGDEVAVLKNNPQ-SITYTDT 183
b 172 KTLLEKPLFFIOACRGTELDG-----IQADSGPINDTDA----NPKYKIPVEADF 219
Y 184 LHIYSTVEGLSVYRDKSGFGTQLTDVFIHKKGSILELTEITRL---MANTEWMOEG 240
b 220 LPAVSTVPGYYSWSPGRSGFWVALCSI-LEEHGKDLIMQLITRVNDVARHPESQSD 278
Y 241 KP-----RKVNPVEQSTLRKKLY 258
b 279 DPHFHKQIPCVVSMLTSLY 300
RESULT 13
ID ICE7_MOUSE STANDARD; PRT; 303 AA.
AC P97864; O08669;
JT 01-NOV-1997 (Rel. 35, Created)
JT 01-NOV-1997 (Rel. 35, Last sequence update)
JT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
DE protease Mch-3).
EN CASP7 OR LICE2.
DC Mus musculus (Mouse).
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
DX NCBI_TaxID=10090;
XN [1]
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RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RL CP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Wortmannin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid.";
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Lee G., Molemans F., Schotte P., van Criekeinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Atschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Diatchenko L., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalobos D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smallus D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves and activates sterol
CC regulatory element binding proteins (SREBPs). Overexpression
CC promotes programmed cell death (By similarity).
CC -!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC or send an email to license@isb-sib.ch).
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EMBL; BC005428; BAH05428.1; -.
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MGD; MGI:109383; Casp7.
InterPro; IPR002138; ICE p10.
InterPro; IPR001309; ICE p20.
InterPro; IPR002398; Peptidase C14.
Pfam; PF00656; Peptidase C14; 1.
PRINTS; PR00376; ILICENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Zymogen; Apoptosis.
PROPEP 1 23
CHAIN 24 198
PROPEP 199 206
CHAIN 207 303
ACT SITE 144 144
BY SIMILARITY.
CONFLICT 10 11
CONFLICT 45 45
CONFLICT 48 49
SEQUENCE 303 AA; 34060 MW; 747787ESDESF744 CRC64;
Query Match 18.9%; Score 254.5; DB 1; Length 303;
Best Local Similarity 32.5%; Pred. No. 3.2e-12;
Matches 76; Conservative 37; Mismatches 90; Indels 31; Gaps 8;
Y 36 REGSEVDMALRMRYLYKFSTKMDPTA---QQFLELDEFQQTIDNNEEVPVSCAFV 92
b 87 RGTGDKAGALFKCFONLGFVTVHNDSCAKQDLRKASEEDHSN-----ACFACV 140
Y 93 LMAHGEGELKGEDEKRWLEDFEVLNNKNCALRGPKVYIIQACRGEHRDPGEELRG 152
b 141 LLSHGREDLIYKD-GVTFPIKOLTAHFRGDRCKTLEKPKLFFIACRGTLEDDG----- 194
Y 153 NEELGDEBELGDEVAVLKNNQS-IPVTDLHYSTVEGVLVSRHDEKSGFIQTLTD 211
b 195 -----IQADSGPINDIDANPRNKIPVEADFLFAYSTVPGYSWRNPGKGSWFVQALCS 247
Y 212 VFTHKKGSIETLTETRL---WANTEVMEQKPR---KVNPEVQSTLRKKLY 258
b 248 I-LNEHGKOLEIMQILTRYNDVRAHFESQSDPRFNKKQIPCMVSNLTUKELY 300
RESULT 14
ED3 CABEL STANDARD; PRT; 503 AA.
C P42573; P45435; Q9SQ04; Q9NAQ8;
T 01-NOV-1995 (Rel. 32, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
E Cell death protein 3 precursor (EC 3.4.22.-).
N CED-3 OR C48D1.2.
S Caenorhabditis elegans.
C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
C Rhabditidae; Peloderinae; Caenorhabditis.
X NCBI_TaxID=6239;
X [1]
P SEQUENCE FROM N.A., AND MUTAGENESIS.
C STRAIN=Bristol N2;
X MEDLINE=94061982; PubMed=8242740;
A Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
T "The C. elegans cell death gene ced-3 encodes a protein similar to
T mammalian interleukin-1 beta-converting enzyme.";
L Cell 75:641-652(1993).
[2]
P REVISION TO 418.
```

```
RA Horvitz H.R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Burton J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVISIONS.
RA Durbin R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: Acts as a cysteine protease in controlling programmed
CC cell death by proteolytically activating or inactivating a
CC substrate protein or proteins, a potential substrate may be ced-4.
CC Alternatively it might directly cause cell death by
CC proteolytically cleaving proteins that are crucial for cell
CC viability.
CC 1- SUBUNIT: Could be a heterodimer of two subunits derived from the
CC precursor sequence by a probable autocatalytic mechanism.
CC 1- DEVELOPMENTAL STAGE: Most abundant during embryogenesis and is
CC also detected at later stages.
CC 1- PTM: May be regulated by phosphorylation.
CC 1- SIMILARITY: Belongs to peptidase family C14.
CC 1- SIMILARITY: Contains 1 CARD domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L29052; AAA27982.2; -.
DR EMBL; AF210702; AAG42045.1; -.
DR EMBL; Z81049; CAB61001.2; -.
DR FIR; A49429; A49429.
DR HSSP; P42574; ICP3.
DR MEROPS; C14.002; -.
DR WormPep; C48D1.2; CE29088.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILICENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
FT CHAIN 1 371
FT CELL DEATH PROTEIN 3 SUBUNIT 1
FT (POTENTIAL).
FT CHAIN 372 503
FT CELL DEATH PROTEIN 3 SUBUNIT 2
FT (POTENTIAL).
FT CARD.
FT DOMAIN 1 91
FT SER-RICH.
FT ACT SITE 304 304
FT BY SIMILARITY.
FT ACT SITE 358 358
FT BY SIMILARITY.
FT MUTAGEN 27 27
FT L->F: IN N1040; LOSS OF FUNCTION.
FT G->R: IN N718; LOSS OF FUNCTION.
FT G->S: IN N2433; LOSS OF FUNCTION.
FT A->V: IN N229/N1164; LOSS OF FUNCTION.
FT A->V: IN N2430; LOSS OF FUNCTION.
FT E->K: IN N2426; LOSS OF FUNCTION.
FT S->F: IN N1163; LOSS OF FUNCTION.
FT MUTAGEN 486 486
FT SSEQUENCE 503 AA; 56616 MW; 722D5831F94DAA69 CRC64;
Query Match 18.7%; Score 253; DB 1; Length 503;
```


Best Local Similarity 28.9%; Pred. No. 7.9e-12;
Matches 69; Conservative 49; Mismatches 101; Indels 20; Gaps 7;
Y 36 REGSEVDMLEALRMFRYLKPFSTMKDPTAQOFLDELDFQOTIDNWEPPVSCAPVUMA 95
b 259 RNGTKADKONLTNLFRCMGVTYICKNLTGRGMILLTIRDFAK---HESHGDSAILVILS 314
Y 96 HGBEGLLKGEDEKMWLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEEELRGNEE 155
b 315 HGBENVIIIGDDTPISTHEIYDILNANPRLANKPKIVFQACGERDNGFFVILDSVD 374
Y 156 -----LGDEBELGG--DEVAVLKNNPQSI-----PTYDTLHIVSTVEGYLSYRHDEKG 202
b 375 GVPAFLRRGWDNRDGLFNLGCVRPQVQWKRKPSQADILAIYATTAQYVWNSARG 434
Y 203 SGPTQLTLDYF-IHKKG-STLELTERITLMA-NTEVMQEGKPKVKNPEVOSTLRKKLY 258
b 435 SWFIQAVCEVFSTHAKMDVVELLTENVKVKVACGFTSGSNNLKQMPENTSRLLKKFY 493
RESULT 15
CE7 MESAU
D -ICE7 MESAU STANDARD; PRT; 303 AA.
C P55214;
Y 01-OCT-1996 (Rel. 34, Created)
Y 01-OCT-1996 (Rel. 34, Last sequence update)
Y 28-FEB-2003 (Rel. 41, Last annotation update)
Y Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
Y (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
Y (SCA-2).
Y CASP7 OR MCH3.
Y Mesocricetus auratus (Golden hamster).
Y Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Y Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Y Mesocricetus.
Y NCBI TaxID=10036;
Y [1]
Y SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
Y STRAIN=Syrian; TISSUE=Liver;
Y MEDLINE=96224303; PubMed=8643593;
Y Pai J.-T., Brown M.S., Goldstein J.L.;
Y "Purification and cDNA cloning of a second apoptosis-related cysteine
Y protease that cleaves and activates sterol regulatory element binding
Y proteins.";
Y Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
Y -!- FUNCTION: Involved in the activation cascade of caspases
Y responsible for apoptosis execution. Cleaves and activates sterol
Y regulatory element binding proteins (SREBPs). Proteolytically
Y cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
Y bond. Overexpression promotes programmed cell death (By
Y similarity).
Y -!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
Y (By similarity).
Y -!- SUBCELLULAR LOCATION: Cytoplasmic.
Y -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
Y SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
Y CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
Y CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
Y VICE VERSA (BY SIMILARITY).
Y -!- SIMILARITY: Belongs to peptidase family C14.
Y
Y This SWISS-PROT entry is copyright. It is produced through a collaboration
Y between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Y or send an email to license@isb-sib.ch).
Y
Y -----
Y EMBL; U47332; AAC52595.1; -.
Y HSP; P42574; 1PAU.
Y MEROPS; C14.004; -.
Y InterPro; IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00456; Peptidase C14; 1.
DR PRINTS; PR00376; ILIIBENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;
Query Match 18.5%; Score 249.5; DB 1; Length 303;
Best Local Similarity 32.2%; Pred. No. 7.6e-12;
Matches 76; Conservative 36; Mismatches 89; Indels 35; Gaps 9;
QY 36 REGSEVDMLEALRMFRYLKPFSTMKDPTA---QOFLDELDFQOTIDNWEPPVSCAPV 92
DB 87 RGTGDKDAELPKCFRSLGFDVVVYNDSCAKWQDLLKASEEDHSNS-----ACPACV 140
QY 93 LMAHGEGLLKGEDEKMWLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEEELRG 152
DB 141 LLSHGSENLTYGKD-GVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTLDGQVQ--- 196
QY 153 NEELGGDEELGGDEVAVLKNNPQ-SIPTVDTLHIVSTVEGYLSYRHDEKSGFTQLTLD 211
DB 197 -ADSGPINETDA-----NPKYKIPVEADFLFAYSTVPGYYSWNEFGKGSFWFOALCS 247
CY 212 VFTHKGSILELTERITLMAANTEVMQEGK-----PRKNPEVOSTLRKKLY 258
DB 248 I-LDEHGKDLIEMQILTRV--NDRVARHFPESCDDPCFNEKKQIPCMVSMILTKEY 300
Search completed: March 19, 2004, 11:22:45
Job time : 11.3586 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: March 19, 2004, 11:18:31 ; Search time 14.502 Seconds
(without alignments)
1724.577 Million cell updates/sec

file: US-09-989-903-2

effect score: 1350

sequence: 1 KPMSEMSDPOPLQERYD.....KPRKVNPEVQSTLRKLYLQ 260

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 283366 seqs, 96191526 residues

total number of hits satisfying chosen parameters: 283366

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

1: piri:*

2: piri:*

3: piri:*

4: piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match %	Length	ID	Description
1	940.5	69.7	242	JC7517	caspase-14/a - hum
2	281	20.8	277	JC5410	CP32 protein - mo
3	274.5	20.3	435	A54821	apoptosis regulato
4	274.5	20.3	452	JC6507	caspase-2 - rat
5	273	20.2	277	A55315	cysteine proteinas
6	268	19.9	454	JC7123	caspase-9 long cha
7	265	19.6	277	S64710	cysteine proteinas
8	255.5	18.9	212	I67437	ICB-LAR6 - human
9	253	18.7	416	G02635	interleukin-1 beta
10	253	18.7	503	A49429	interleukin-1 beta
11	231.5	17.1	495	T20038	hypothetical prote
12	219	16.2	182	I67436	interleukin-1-beta
13	215.5	16.0	311	B56084	interleukin-1-beta
14	215.5	16.0	383	A56084	interleukin-1-beta
15	215.5	16.0	404	A42577	interleukin-1 beta
16	203	15.0	418	B57511	interleukin-1 beta
17	201.5	14.9	402	A46495	IL-1 beta converta
18	200	14.8	312	B54821	apoptosis regulato
19	190.5	14.1	377	A57511	interleukin-1 beta
20	188.5	14.0	263	C56084	interleukin-1-beta
21	186	13.8	826	T43638	caspase-related pr
22	156	11.6	536	T43638	caspase-related pr
23	154	11.4	488	T13385	hypothetical prote
24	147.5	10.9	642	T27021	hypothetical prote
25	142	10.5	136	T53300	interleukin-1-beta
26	102	7.6	1429	S16233	nitric-oxide synth
27	99	7.3	505	S39520	H+-transporting tw
28	97.5	7.2	819	T19351	hypothetical prote
29	96.5	7.1	248	C62376	amino acid ABC tra

30	95.5	7.1	843	2	A47132	major vault protei
31	95.5	7.1	880	2	F75103	conserved hypothet
32	94.5	7.0	1095	2	PC1114	SKDC25 protein -
33	94	7.0	617	2	D96978	hypothetical prote
34	94	7.0	1875	2	S38173	myosin-like protei
35	93.5	6.9	747	2	D95862	probable sensor hi
36	93	6.9	544	2	A42464	microbial metallo
37	92.5	6.9	952	2	D86179	hypothetical prote
38	92.5	6.9	1093	2	A31758	phosphorylase kina
39	92.5	6.9	1093	2	B40793	phosphorylase kina
40	92.5	6.9	1156	2	B70356	chromosome assembl
41	92	6.8	700	2	E69146	sensory transducti
42	91.5	6.8	489	2	S17813	ctdJ protein - Rho
43	91.5	6.8	1920	2	A53188	pericentrin - mous
44	91.5	6.8	2670	2	A46719	inositol 1,4,5-tri
45	91	6.7	971	2	A70179	exodeoxyribonuclea

ALIGNMENTS

RESULT 1

JC7517

caspase-14/a - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C/Accession: JC7517

R/Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.

Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A/Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyte

A/Reference number: JC7517; MUID:20517231; PMID:11062009

A/Contents: Epidermal keratinocytes

A/Accession: JC7517

A/Molecule type: mRNA

A/Residues: 1-242 <ECK>

A/Cross-references: GB:AF097874

C/Comment: This enzyme accumulates during keratinocyte differentiation and is activated

C/Genetics:

A/Gene: casp-14/a

A/Map position: 19p13.1

A/Introns: 9/3; 59/3; 135/1; 174/1; 208/3

C/Keywords: differentiation

Query Match	69.7%	Score	940.5	DB	2	Length	242
Best Local Similarity	71.3%	Pred. No.	2.2e-63				
Matches	181	Conservative	31	Mismatches	29	Indels	13
Gaps	2						
Qy	8	MSDPQLQERYDMSGARLALITLVTKAREGSEVDMERALERYLYKFEETMKEDPTAQQ	67				
Db	1	MSNPSLEEEKYDMSGARLALITLVTKAREGSEEDLDALAHNFQLRFESTMKEDPTAEQ	60				
Qy	68	FLEELDEFQOTIDNNEEPVSCAFVVLMAHGEGGLKGEDEKVRLEDLFEVLNNKCKAL	127				
Db	61	FQEELEKFOQADSREDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL	120				
Qy	128	RGPKVYIIQACRGHRDPGEELRGNEELGGDEELGGDE-VAVLKNPQSPITVTDLIHI	186				
Db	121	RAPKPVYIIQACRGGEORDFG-----ETVGGDEIVVMVINKDSQTIPTVTDALHV	169				
Qy	187	YSTVEGVLVSRHDEKSGGFIQTLTVFIHKSGISILEETETRLMANTENVMOEGKPRVN	246				
Db	169	YSTVEGIYIARHDKSGSCFIQTLVDVFKRKSHILLELLETVTRMAELVQEGKARKTN	228				
Qy	247	PEVQSTLRKLYLQ 260					
Db	229	PEIQSTLRKRLYLQ 242					

RESULT 2

JC5410

CP32 protein - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999

```

;Accession: JC5410
;Mukasa, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
;iochem. Biophys. Res. Commun. 231, 770-774, 1997
;Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation
;Reference number: JC5410; MUID:97224429; PMID:9070890
;Accession: JC5410
;Status: nucleic acid sequence not shown
;Molecule type: mRNA
;Residues: 1-277 <NUK>
;Cross-references: DDBJ:D86352
;Experimental source: embryo
;Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match      20.8%; Score 281; DB 2; Length 277;
Best Local Similarity 30.8%; Pred. No. 7,6e-14;
Matches 82; Conservative 45; Mismatches 91; Indels 48; Gaps 10;

y 16 ERYDNGSARLALTCVT-----KAREGEVDMEALRFRYLKPESTMKRDPPTA 65
b 34 DSSYKMDYEMGICITIKNPKHSTGMSRSRGTVDVAANLRETFTMGLKYEVRNKNLDR 93
y 66 QQFLBELDFQOTIDNWEPEVSCAFV-VLMAHGEGLKGEDEKMKVRLDLFEVLNNKNC 124
b 94 EELMELND-----SVSKEDSKRSSFVCVILSHGDEGVIFGNGP-VDLKLTFFRGDYC 148
y 125 KALRGKPKYVYIIQACRGEHRDPGEELRGNELGGDEELGGDEVAVLKNNPQSIPYTTDL 184
b 149 RSLTGKPKFLIIQACRGTDLDOGIE---TDSGTDEMA-----CQKIPVEADFL 194
y 185 HYISTVEGYLSVRHDEKSGFTQTLTD---VFPHKKGSIILBTEITRLMANTVEMQEGK 241
b 195 YAYSTAPGYYSWRNKGDSWFFQISCSMLKYAHK-----LEFMILTRV--NRKVATEPE 248
y 242 -----PRKVNPEVQSTLRKKLY 258
b 249 SFSLDSTPHAKQIPCVISMLTKELY 274

RESULT 3
54821
poptosis regulator ICH-1, stimulatory form L - human
;Species: Homo sapiens (man)
;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
;Accession: A54821
;Wang, L.; Mura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
;ell 78, 739-750, 1994
;Title: ICH-1, an ICE/CED-3-related gene, encodes both positive and negative regulators
;Reference number: A54821; MUID:94373611; PMID:8087842
;Accession: A54821
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-435 <WAN>
;Cross-references: GB:U13021; NID:9537291; PID:9537292
;Keywords: alternative splicing; apoptosis

Query Match      20.3%; Score 274.5; DB 2; Length 435;
Best Local Similarity 29.7%; Pred. No. 4.1e-13;
Matches 66; Conservative 51; Mismatches 103; Indels 7; Gaps 4;

y 36 REGSEVDMEALRFRYLKPESTMKRDPPTAQQLFLELDEFQOTIDNWEPEVSCAFVILMA 95
b 202 RSGGDVHSTLVTFLKLLGYDVHVLCDQTAQEMQEKLNQFAQ-LPAHRVTDSC-IVALLS 259
y 96 HGEGLLKGDEKMKVRLDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEELRGNEE 155
b 260 HGVEGAIYGVGDKLLQLQEVFQLFDNANCPSLQNKPKMFFIACRGDETDGRGVQDQGN 319
y 156 LGGDEELGGDEVAVLKNNPQSIPYTTDLTHYSTVEGYLSVRHDEKSGFTQTLTDVFIH 215
b 320 HAGSPGCEESDAGKELPKMRLPTRSDMICGACLKGNAAAMRTKRGSWYIEALQVFESE 379
y 216 KKGGS--LLELTEETRLMANTVEMQEGK---RKVNPEVQSTLRKKLYL 259

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Db 380 PACDMHVADMLVKVNALIKDREGVAPGTGFHRCKEMSEYCVSTLCRHLYL 428

RESULT 4
JC6507
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC6507
R:Sato, N.; Milligan, C.B.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202, 127-132, 1997
A:Title: Cloning and expression of the cDNA encoding rat caspase-2.
A:Reference number: JC6507; MUID:98087427; PMID:9427555
A:Accession: JC6507
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <SAT>
A:Cross-references: GB:U79933; NID:92769705; PIDN:AA96379.1; PID:92769706

Query Match      20.3%; Score 274.5; DB 2; Length 452;
Best Local Similarity 30.6%; Pred. No. 4.3e-13;
Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

Qy 36 REGSEVDMEALRFRYLKPESTMKRDPPTAQQLFLELDEFQOTIDNWEPEVSCAFVILMA 95
Db 219 RSGGDVHSTLVTFLKLLGYDVHVLCDQTAQEMQEKLNQFAQ-LPAHRVTDSC-IVALLS 276
Qy 96 HGEGLLKGDEKMKVRLDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPG---BELRG 152
Db 277 HGVEGAIYGVGDKLLQLQEVFQLFDNANCPSLQNKPKMFFIACRGDETDGRGVQDQGN 336
Qy 153 NEEELGGDEELGGDEVAVLKNNPQSIPYTTDLTHYSTVEGYLSVRHDEKSGFTQTLTDV 212
Db 337 HAQSPGCEESDAGKEELMK---MELPTRSDMICGACLKGNAAAMRTKRGSWYIEALTQV 393
Qy 213 FIHKKGGS--LLELTEETRLMANTVEMQEGK---RKVNPEVQSTLRKKLYL 259
Db 394 FSRACDMHVADMLVKVNALIKREGVAPGTGFHRCKEMSEYCVSTLCQQLYL 445

RESULT 5
A55315
cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human
N:Alternate names: cysteine proteinase CPP32
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C:Accession: A55315; S58999; I39005
R:Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A:Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans C
A:Reference number: A55315; MUID:95074098; PMID:7983002
A:Accession: A55315
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-277 <FER>
A:Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666
R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.
; Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian
A:Reference number: S58999; MUID:95319529; PMID:7596430
A:Accession: S58999
A:Molecule type: protein
A:Residues: 29-46; 176-189, 'E', 191-193 <NIC>
R;Rewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Poirier,
Cell 81, 801-809, 1995
A:Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease th
A:Reference number: A56924; MUID:95292347; PMID:7774019
A:Accession: I39005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-189, 'E', 191-277 <RES>
A:Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569

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;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 20.28; Score 273; DB 2; Length 277;
 Best Local Similarity 31.58; Pred. No. 3e-13;
 Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;
 Y 6 SEMSDPQAEYDMSGARLATLCTVK-----AREGSEVDMEALRMFRYLKFP 55
 Y 24 SESMDSGISLDSYKMDYPMGLCIINNNKFNHKTGCTSRGCTDVAANLRETFNRLKY 83
 Y 56 ESTMKRPTAQQLFELDEFOQIDNWEVPVSCAFV-VLMAHGEGLLKGDEKVRLED 114
 Y 84 EVRNKNDLTR-----EEIVELMRDVSDEKHSRFSFVCLVLSHGEGLIIFGTNGP-VDLKK 138
 Y 115 LFEVLNNKCKALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEBELGGDEAVLKNKP 174
 Y 139 ITNFRGDRCSRSLTGKPLFIQACRGTDLDCGIE-----TDSGVD-----DDMACHK--- 186
 Y 175 QSIPTYTDLHIYSTVEGYLSYRDEKSGSFQITLTDVPHKKGSIETLCTEITRLMANT 234
 Y 197 --IPVDADFLYAVSTAGYYSWRNSKDGSWFIQSLC-AMLKQYADKLFPNHLITRV--NR 241
 Y 235 EVMQEGK-----PRKVNPEVQSTLRKKLY 258
 Y 242 KVATEFESFSDATFPAKQKQIPCIVSMLTKEY 274

RESULT 6

JC7123
 ;Species: long chain - mouse
 ;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
 ;Accession: JC7123
 ;Title: Mus musculus (house mouse)
 ;Biochem. Biophys. Res. Commun. 264, 550-555, 1999
 ;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
 ;Reference number: JC7123; MUID:20001956; PMID:10529400
 ;Accession: JC7123
 ;Status: preliminary
 ;Molecule type: mRNA
 ;Residues: 1-454 <FU>
 ;Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

Query Match 19.9%; Score 268; DB 2; Length 454;
 Best Local Similarity 30.2%; Pred. No. 1.3e-12;
 Matches 74; Conservative 45; Mismatches 96; Indels 30; Gaps 8;
 Y 36 REGSEVDMEALRMFRYLKPESTMKRDPDTAQQLFELDEFOQIDNWEVPVSCAFVVLMA 95
 Y 218 RTGSDNRDKLEHFRMLRFNMFVEKNDLTAKQVYALMMAH---RNHRALDCFVVVILS 274
 Y 96 HGE-----GLLKGDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPGE 148
 Y 275 HGCASHLQFFGAVYGTGCVSIEKIVNIFNGSGCPSLGKPKLFIQACGGEQKHGF 334
 Y 149 ELRGNEELG-----GDEELGGDEAVLKNKPQ-----SITYTDLHIYSTVEGYLS 195
 Y 335 EVACTSSQGRITLDSSE---PDATFQEGRPRLDQDAVSSLTPSDILVSYSTPFGVS 391
 Y 196 YRHDEKSGSFQITLTDVPHKKGSIETLCTEITRLMANTVMOEGKPRKVNPEVQSTLRK 255
 Y 392 WRDKSGSWYIETLDGILFQWARS--EDLQSLLRVANA-VSEKGYKQI-PCCFNPLRK 447
 Y 256 KLYLQ 260
 Y 448 KLPFK 452

RESULT 7

364710
 ;Species: Chinese hamster
 ;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999

C;Accession: S64710; S72395
 R;Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
 EMBO J. 15, 1012-1020, 1996
 A;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
 A;Reference number: S64710; MUID:96183185; PMID:8605870
 A;Accession: S64710
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-277 <WAW>
 A;Cross-references: EMBL:U27463
 R;Wang, X.
 submitted to the EMBL Data Library, May 1995
 A;Reference number: S72395
 A;Accession: S72395
 A;Molecule type: mRNA
 A;Residues: 1-79, 'A', 81-146, 'Y', 148-277 <WAW>
 A;Cross-references: EMBL:U27463; NID:g1244443; PID:AAB01511.1; PID:g1244444
 C;Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 19.6%; Score 265; DB 2; Length 277;
 Best Local Similarity 33.1%; Pred. No. 1.2e-12;
 Matches 78; Conservative 35; Mismatches 85; Indels 38; Gaps 9;
 Y 36 REGSEVDMEALRMFRYLKPESTMKRDPDTAQQLFELDEFOQIDNWEVPVSCAFV-VLM 94
 Y 64 RSGTDVDAKRLRETFMNLKYEVRNKNLDR-----EEIVELMKNASKEDHSKRSSFVCVIL 119
 Y 95 AHGEGLLKGDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPGEELRGNE 154
 Y 120 SHGDEGVIFGTDPG-IDLKXLTASYPRGDCRSLGKPLFIQACRGTDLDCGIEHDSGT 178
 Y 155 ELGGDEELGGDEAVLKNKPQSIPTYTDLHIYSTVEGYLSYRDEKSGSFQITLTD--- 211
 Y 179 E-----DDMTC-----QKIPVADFLYAVSTAGYYSWRNPKDGSWFIQSLCSMLK 224
 Y 212 VFHKKGSIETLCTEITRLMANTVMOEGK-----PRKVNPEVOSTLRKKLY 258
 Y 225 LYAHK-----LEFMHLITRV--NRKVATEFESFSLDSTPAKQKQIPCIVSMLTKEY 274

RESULT 8

167437
 ;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 A;Accession: 167437
 R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirschfield, A.N.; Til
 Endocrinology 136, 5042-5053, 1996
 A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
 lulosa cells of the ovarian follicle.
 A;Reference number: 153300; MUID:96042508; PMID:7588240
 A;Accession: 167437
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-212 <BS>
 A;Cross-references: EMBL:U34685; NID:g1004370; PID:NAC52261.1; PID:g1004371
 C;Keywords: cysteine proteinase; hydrolase

Query Match 18.9%; Score 255.5; DB 2; Length 212;
 Best Local Similarity 31.4%; Pred. No. 4.5e-12;
 Matches 72; Conservative 38; Mismatches 82; Indels 37; Gaps 9;
 Y 16 EERYDMSGARLATLCTV-----KARGSEVDMEALRMFRYLKPESTMKRDPDTA 65
 Y 5 DSSYKMDYPMGLCIINNNKFNHKTGCTSRGCTDVAANLRETFMALRYEVRNKNLDR 64
 Y 66 QQFLFELDEFOQIDNWEVPVSCAFV-VLMAHGEGLLKGDEKVRLEDLFEVLNNKNC 124
 Y 65 EEIMELMD-----SVSKEDHSKRSSFVCVILSHGDEGVIFGTNGP-VDLKLTSTFFRGDYC 119
 Y 125 KALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEBELGGDEAVLKNKPQSIPTYTDL 184
 Y 120 RSLTGKPKLFIQACRGTDLDSGIE-----TDSGAD-----DDVACQKK-----PVEADFL 165


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>Molecule type: mRNA
>Residues: 1-182 <RES>
>>Cross-references: EMBL:U34684; NID:g1004368; PIDN:AACS2260.1; PID:g1004369

Query Match          16.2%; Score 219; DB 2; Length 182;
Best Local Similarity 32.1%; Pred. No. 2e-09;
Matches 51; Conservative 39; Mismatches 61; Indels 8; Gaps 4;

iy 36 REGSEVDEALERMFYKPFESTMKDPTAQOFLBELDEFQOTIDNWEEPVSCAVVIMA 95
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
ib 22 RSGGDVDHTTTLVTLFKLGNVHVLYDOTAQEWQEKLNFAQLPAHRVTDSC-IVALLS 79
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
iy 96 HGERGLKGDEKMWRLLEDLFVLNNKNCKALRGPKVYIIQACRGEHDPG---EELRG 152
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
ib 80 HGVEGGIYGVDGKKLLQEQEVRIUDFNANPQSQNPKQFFFOACKRGDETDRGVDDQDGKN 139
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
iy 153 NEELGGDEELGGDEVAVLKNNPOSIPITYDTDLHIYSTVE 191
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
ib 140 HAQPPGCCESDVTKEBLWK--MRLPTRSDMICVYACLK 175
      |||::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 13
AS56084
interleukin-beta converting enzyme gamma isozyme - human
C:Species: Homo sapiens (man)
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
C:Accession: B56084
C:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
A>Title: Cloning and expression of four novel isoforms of human interleukin-beta conver
A:Reference number: A56084; MUID:95181414; PMID:7876192
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-311 <LAN>
A:Cross-references: GB:U13698; NID:g717041; PIDN:AACS0108.1; PID:g717042
A:Genetics:
A:Gene: IL1BCE
A:Keywords: alternative splicing

Query Match          16.0%; Score 215.5; DB 2; Length 311;
Best Local Similarity 30.3%; Pred. No. 7.2e-09;
Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

iy 22 SGARLATLCVTK-----AREGSEVDEALERMFYKPFESTMKRDPTAQOFLBELDEP- 75
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
ib 67 SRTLRALIICNEEFDSIPRRTAGVDITGTMTLNLQNLGYSDVKXNLTASDWTTELEAFA 126
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
iy 76 ----COOTDNWEEPVSACFVYLVAHG-EEGILL-KGEDEX---MWRELDLFVLNNKNCKA 126
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
ib 127 HRPEKTSDS-----TFILVFMSHGIREGICKGHSEQVPDIQLQINAFNMNLNTKNCP 179
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
iy 127 LRGPCKPVIIQACRGEHDPG-----EBLRNHEELGGDEELGGDEVAVLKNNPOSIPT 179
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
ib 180 LKDQKPVIIQACRGD--SPGVWFKDSVGSNCLSLPTEEFEED--AIKKAHEK---- 232
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
iy 180 YDTDLHIYSTVEGYLSTRHBEKSGFTQTITDVFIHKKSILEL-TETITRLMANTEVWQ 238
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
ib 233 ---DFIAFCSSPTPDNVSWRHPTMGVSFTGRLLIE---HMQEYACSDVEEIFRKVRFSBP 287
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
iy 239 EGKPKKVNPVEQSTLRKKLYL 259
      |||::||::||::||::||::||::||::||::||::||::||::||::||:
ib 288 DGRAQMPTTE-RVILTTRCFYL 307
      |||::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 14
AS56084
interleukin-beta converting enzyme beta isozyme - human
C:Species: Homo sapiens (man)
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
C:Accession: A56084
C:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995

```

```
;Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves
;Reference number: S24164; MUID:192337439; PMID:1321594
;Accession: S24164
;Status: preliminary
;Molecule type: protein
;Residues: 120-135,'AX',138-139,'X',141-142 <KRO>
;Genetics:
;Gene: GDB:IL1BC
;Cross-references: GDB:132368; OMIM:147678
;Map position: 11q23-11q23
;Keywords: cysteine proteinase; hydrolase

Query Match      16.0%; Score 215.5; DB 2; Length 404;
Best Local Similarity 30.3%; Pred. No. 1e-08;
Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

y 22 SGARLALTLCVTK-----AREGSEVDMEMALERMFRYLAFESTMKDPTAQOFLDELDEF- 75
b 160 SRTFLALIIICNEEFDSIPRRTGAEDITGMTLLQLNLGYSDVKKNLTASDMTTTELEAFA 219

y 76 ---QOTIDNWEPEVSCAFVILMAHG-BEGLL-KGEDEK--MVRLEDLFEVLNNKNCKA 126
b 220 HREHKTSDS-----TLVFMHSHGIRGICGKKHSEQVPDILQLNAIFNMLATKNCP 272

y 127 LRQKPKYIIQACRGEHRDPG-----BELRGNBELGGDEELGGDEVAVLKNPQSIPT 179
b 273 LRQKPKYIIQACRGEHRDPG-----BELRGNBELGGDEELGGDEVAVLKNPQSIPT 179

y 180 YTDLTHIYSTVEGYLSYRDEKSGFGIOTLDVFIHKKSILEL--TEBITRLMANTVW 238
b 326 --DFIACSTPDNVSWRHPTWGSVFIQRLIE--HMGEYACSDVEIFRKYRFSPEQP 380

y 239 EGKPRKVNPEVOSTLRKKYL 259
b 381 DGRAQMPTE-RVTLTRCFYL 400
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Search completed: March 19, 2004, 11:24:51
ob time : 15.502 secs

GenCore version 5.1.6
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WM protein - protein search, using sw model

Run on: March 19, 2004, 11:24:16 ; Search time 36.7729 Seconds

(without alignments)
1830.924 Million cell updates/sec

Title: US-09-989-903-2

Perfect score: 1350

Sequence: 1 KPDMESEMSDPQLQERYD.....KPKVNPEVQSLTKLYLQ 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pap.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pap.*
6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pap.*
7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pap.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pap.*
9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pap.*
10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pap.*
11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	260	9	US-09-989-903-2
2	1350	100.0	260	14	US-10-068-564-2
3	1332	99.7	257	9	US-09-764-803A-2
4	1313	97.3	253	15	US-10-114-432-29
5	968	71.7	185	15	US-10-114-432-35
6	940.5	69.7	242	9	US-09-845-028-2
7	940.5	69.7	242	10	US-09-851-873-105
8	940.5	69.7	242	15	US-10-114-432-3
9	940.5	69.7	242	15	US-10-114-432-15
10	940.5	69.7	242	15	US-10-114-432-17
11	940.5	69.7	242	15	US-10-114-432-18
12	940.5	69.7	242	15	US-10-114-432-26
13	940.5	69.7	242	15	US-10-114-432-27
14	940.5	69.7	242	15	US-10-114-432-28
15	940.5	69.7	242	15	US-10-114-432-30

16	940.5	69.7	242	15	US-10-114-432-31	Sequence 31, Appl
17	940.5	69.7	242	15	US-10-114-432-67	Sequence 67, Appl
18	940.5	69.7	242	15	US-10-114-432-69	Sequence 69, Appl
19	940.5	69.7	242	15	US-10-114-432-71	Sequence 71, Appl
20	940.5	69.7	242	15	US-10-114-432-73	Sequence 73, Appl
21	938.5	69.5	242	15	US-10-114-432-13	Sequence 13, Appl
22	938.5	69.5	242	15	US-10-114-432-23	Sequence 23, Appl
23	935.5	69.3	241	15	US-10-114-432-37	Sequence 37, Appl
24	934.5	69.2	242	9	US-09-989-903-5	Sequence 5, Appl
25	934.5	69.2	242	14	US-10-068-564-5	Sequence 5, Appl
26	928.5	68.8	242	15	US-10-114-432-11	Sequence 11, Appl
27	928.5	68.8	242	15	US-10-114-432-22	Sequence 22, Appl
28	921.5	68.3	321	15	US-10-114-432-36	Sequence 36, Appl
29	921.5	68.3	321	15	US-10-114-432-9	Sequence 9, Appl
30	921.5	68.3	321	15	US-10-114-432-21	Sequence 21, Appl
31	921.5	68.3	321	15	US-10-114-432-66	Sequence 66, Appl
32	921.5	68.3	321	15	US-10-114-432-72	Sequence 72, Appl
33	912.5	67.6	242	9	US-09-764-803A-24	Sequence 24, Appl
34	912.5	67.6	242	9	US-09-845-028-9	Sequence 9, Appl
35	892.5	66.1	229	9	US-09-764-803A-4	Sequence 4, Appl
36	804.5	59.6	214	9	US-09-989-903-9	Sequence 9, Appl
37	804.5	59.6	214	14	US-10-068-564-9	Sequence 34, Appl
38	692.5	51.3	174	15	US-10-114-432-34	Sequence 7, Appl
39	692.5	51.3	230	9	US-09-989-903-7	Sequence 7, Appl
40	692.5	51.3	230	14	US-10-068-564-7	Sequence 5, Appl
41	692.5	51.3	230	15	US-10-114-432-5	Sequence 19, Appl
42	692.5	51.3	230	15	US-10-114-432-19	Sequence 64, Appl
43	692.5	51.3	230	15	US-10-114-432-64	Sequence 68, Appl
44	692.5	51.3	230	15	US-10-114-432-68	Sequence 32, Appl
45	553	41.0	134	15	US-10-114-432-32	

ALIGNMENTS

RESULT 1

US-09-989-903-2
; Sequence 2, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-2

Query Match 100.0%; Score 1350; DB 9; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.3e-122;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	KPDMESEMSDPQLQERYDMSGARLALTLCTVKAREGSEVDMEALERMFYLLKPESTMK	60
DB	1	KPDMESEMSDPQLQERYDMSGARLALTLCTVKAREGSEVDMEALERMFYLLKPESTMK	60
QY	61	RDPTAQOFLBELDEFQOTIDNWEVPVSCAFVVLMAHGESGLKGEDEKVRLEDLFEVLN	120
DB	61	RDPTAQOFLBELDEFQOTIDNWEVPVSCAFVVLMAHGESGLKGEDEKVRLEDLFEVLN	120
QY	121	NNCKALRGPKVYIIOACRGEHRDPGEELRGNEELGGDEELGGDEAVLKNPPOSITPY	180
DB	121	NNCKALRGPKVYIIOACRGEHRDPGEELRGNEELGGDEELGGDEAVLKNPPOSITPY	180
QY	181	TDTLHYSTVEGYSYLRHDEKSGFGTQTLTDVFIHKGSILETEITRLMANTVEMQSG	240

b 181 TDTLHIYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEG 240
y 241 KPRKVNPEVQSTLRKKLYIQ 260
b 241 KPRKVNPEVQSTLRKKLYIQ 260

RESULT 2
S-10-068-564-2
Sequence 2, Application US/10068564
Publication No. US20030040096A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C2
CURRENT APPLICATION NUMBER: US/10/068,564
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
S-10-068-564-2

Query Match 100.0%; Score 1350; DB 14; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.3e-122;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 KPDMESEMSDPOQLQEERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMK 60
b 1 KPDMESEMSDPOQLQEERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMK 60
y 61 RDPTAQOQFLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKXVRLDLEVLN 120
b 61 RDPTAQOQFLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKXVRLDLEVLN 120
y 121 NKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEGVAVLKNPQSIPTY 180
b 121 NKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEGVAVLKNPQSIPTY 180
y 181 TDTLHIYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEG 240
b 181 TDTLHIYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEG 240
y 241 KPRKVNPEVQSTLRKKLYIQ 260
b 241 KPRKVNPEVQSTLRKKLYIQ 260

RESULT 3
US-09-764-803A-2
Sequence 2, Application US/09764803A
Patent No. US20020034812A1
GENERAL INFORMATION:
APPLICANT: Van de Craen, Marc
APPLICANT: Declercq, Wim
APPLICANT: Vandenabeele, Peter
APPLICANT: Fiers, Walter
TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
FILE REFERENCE: 2676-4661US
CURRENT APPLICATION NUMBER: US/09/764,803A
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: PCT/EP99/04939
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: EP 98202422.6
PRIOR FILING DATE: 1999-07-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 257

Query Match 97.3%; Score 1313; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 8.5e-119;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 8 MSDPQPLQEERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMKDPTAQ 67
b 1 MSDPQPLQEERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMKDPTAQ 60
y 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKXVRLDLEVLNKNCKAL 127
b 61 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKXVRLDLEVLNKNCKAL 120
y 128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEGVAVLKNPQSIPTYDTHIY 187
b 121 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEGVAVLKNPQSIPTYDTHIY 180
y 188 STVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEGPKNP 247
b 188 STVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEGPKNP 247

TYPE: PRT
ORGANISM: Mus musculus
US-09-764-803A-2

Query Match 98.7%; Score 1332; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.2e-120;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MESEMSDPOQLQEERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMKRDP 63
DB 1 MESEMSDPOQLQEERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMKRDP 60
QY 64 TAOQFLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKXVRLDLEVLNKN 123
DB 61 TAOQFLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKXVRLDLEVLNKN 120
QY 124 CKALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEGVAVLKNPQSIPTYTDT 183
DB 121 CKALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEGVAVLKNPQSIPTYTDT 180
QY 184 LHIYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEGKPR 243
DB 181 LHIYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEGKPR 240
QY 244 KVNPEVQSTLRKKLYIQ 260
DB 241 KVNPEVQSTLRKKLYIQ 257

RESULT 4
US-10-114-432-29
Sequence 29, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Chailita-Sid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Ava
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 253
TYPE: PRT
ORGANISM: Mus musculus
US-10-114-432-29

181 STVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILETTEITRLMANTVMOEGKPRKYNP 240
248 EVOSTLRKKLYLQ 260
241 EVQSTLRKKLYLQ 253

RESULT 5
US-10-114-432-35
Sequence 35, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Fakis, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovics, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114.432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 185
TYPE: PRT
ORGANISM: Mus musculus
US-10-114-432-35

Query Match 71.7%; Score 968; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.4e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 67
Db 1 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 60

2Y 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 127
Db 61 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 120

2Y 128 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 187
Db 121 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 180

2Y 188 STVEG 192
Db 181 STVEG 185

RESULT 6
US-09-845-028-2
Sequence 2, Application US/09845028
Patent No. US20020081705A1
GENERAL INFORMATION:
APPLICANT: Mankovich, John
TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
FILE REFERENCE: BBI-111
CURRENT APPLICATION NUMBER: US/09/845.028
CURRENT FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/199,962
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-09-845-028-2

Query Match 69.7%; Score 940.5; DB 9; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

2Y 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 67
Db 1 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 60

2Y 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 127
Db 61 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 120

2Y 128 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 186
Db 121 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 168

2Y 187 YSTVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILETTEITRLMANTVMOEGKPRKYN 246
Db 169 YSTVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILETTEITRLMANTVMOEGKPRKYN 228

247 PEVQSTLRKKLYLQ 260
229 PEIQSTLRKKLYLQ 242

RESULT 8
US-10-114-432-3

Query Match 69.7%; Score 940.5; DB 9; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

QY 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 67
Db 1 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 60

QY 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 127
Db 61 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 120

QY 128 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 186
Db 121 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 168

QY 187 YSTVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILETTEITRLMANTVMOEGKPRKYN 246
Db 169 YSTVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILETTEITRLMANTVMOEGKPRKYN 228

247 PEVQSTLRKKLYLQ 260
229 PEIQSTLRKKLYLQ 242

RESULT 7
US-09-851-873-105
Sequence 105, Application US/09851873
Publication No. US20030165488A1
GENERAL INFORMATION:
APPLICANT: Kletzien, Rolf F
APPLICANT: Weiland, Katherine L
TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
FILE REFERENCE: 28341/00233
CURRENT APPLICATION NUMBER: US/09/851.873
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-873-105

Query Match 69.7%; Score 940.5; DB 10; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

QY 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 67
Db 1 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 60

QY 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 127
Db 61 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 120

QY 128 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 186
Db 121 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 168

QY 187 YSTVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILETTEITRLMANTVMOEGKPRKYN 246
Db 169 YSTVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILETTEITRLMANTVMOEGKPRKYN 228

247 PEVQSTLRKKLYLQ 260
229 PEIQSTLRKKLYLQ 242

Query Match 69.7%; Score 940.5; DB 10; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

QY 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 67
Db 1 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTWKRPDTAQ 60

QY 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 127
Db 61 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKCKAL 120

QY 128 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 186
Db 121 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEVAVLKNNPQSIPTTYDTLHI 168

QY 187 YSTVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILETTEITRLMANTVMOEGKPRKYN 246
Db 169 YSTVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILETTEITRLMANTVMOEGKPRKYN 228

247 PEVQSTLRKKLYLQ 260
229 PEIQSTLRKKLYLQ 242

RESULT 8
US-10-114-432-3

Sequence 3, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Bid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

S-10-114-432-3

Query Match 69.7%; Score 940.5; DB 15; Length 242;

Best Local Similarity 71.3%; Pred. No. 9.7e-83;

Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

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Y 8 MSDPQLQEEYDMGARGALALTLCTVKAREGSEVDMEALERMFRYLKPESTMKRDPTAQ 67
b 1 MSNPRSEEEKYDMGARGALALTLCTVKAREGSEEDLDALHMFRLQRFESTMKRDPTAQ 60
Y 68 FLEELDFEQTIDNWEPEVSCAFVVLMAHGEGLKGEDEKMWLEDFEVLNKNCKAL 127
b 61 FQEELEKFOQAIDSRDPSVCAVFLMAHGREGLKGEDEGMVKLENLFEALNNKCOAL 120
Y 128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPQSIPTVDTLHI 186
b 121 RAKPKVYIIQACRGEQDPG-----ETVGGDEIVMWIKDSPQTIPTVTDALHV 168
Y 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKGSIIELTEETRLMANTVWQEGPKVN 246
b 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRKHILLELLETVTRMAEALVQEGKARKTN 228
Y 247 PEVOSTLRKLYLQ 260
b 229 PEIQSTLRKLYLQ 242
```

ESULT 9

S-10-114-432-15

Sequence 15, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Bid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 15

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-114-432-15

Query Match 69.7%; Score 940.5; DB 15; Length 242;

Best Local Similarity 71.3%; Pred. No. 9.7e-83;

Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

```
QY 8 MSDPQLQEEYDMGARGALALTLCTVKAREGSEVDMEALERMFRYLKPESTMKRDPTAQ 67
DB 1 MSNPRSEEEKYDMGARGALALTLCTVKAREGSEEDLDALHMFRLQRFESTMKRDPTAQ 60
QY 68 FLEELDFEQTIDNWEPEVSCAFVVLMAHGEGLKGEDEKMWLEDFEVLNKNCKAL 127
DB 61 FQEELEKFOQAIDSRDPSVCAVFLMAHGREGLKGEDEGMVKLENLFEALNNKCOAL 120
QY 128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPQSIPTVDTLHI 186
DB 121 RAKPKVYIIQACRGEQDPG-----ETVGGDEIVMWIKDSPQTIPTVTDALHV 168
QY 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKGSIIELTEETRLMANTVWQEGPKVN 246
DB 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRKHILLELLETVTRMAEALVQEGKARKTN 228
QY 247 PEVOSTLRKLYLQ 260
DB 229 PEIQSTLRKLYLQ 242
```

RESULT 10

US-10-114-432-17

Sequence 17, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Bid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-114-432-17

Query Match 69.7%; Score 940.5; DB 15; Length 242;

Best Local Similarity 71.3%; Pred. No. 9.7e-83;

Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

```
QY 8 MSDPQLQEEYDMGARGALALTLCTVKAREGSEVDMEALERMFRYLKPESTMKRDPTAQ 67
DB 1 MSNPRSEEEKYDMGARGALALTLCTVKAREGSEEDLDALHMFRLQRFESTMKRDPTAQ 60
QY 68 FLEELDFEQTIDNWEPEVSCAFVVLMAHGEGLKGEDEKMWLEDFEVLNKNCKAL 127
DB 61 FQEELEKFOQAIDSRDPSVCAVFLMAHGREGLKGEDEGMVKLENLFEALNNKCOAL 120
QY 128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPQSIPTVDTLHI 186
DB 121 RAKPKVYIIQACRGEQDPG-----ETVGGDEIVMWIKDSPQTIPTVTDALHV 168
QY 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKGSIIELTEETRLMANTVWQEGPKVN 246
DB 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRKHILLELLETVTRMAEALVQEGKARKTN 228
```

```

; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114.432

```

```
b 121 RAKPKYIIQACRGEQDPG-----ETVGGDEIYVMWIKDSPTIPTYTDALHV 168
y 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKKGSIIELEETETRLMANTVNMQEGKPRKVN 246
b 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRGHILELLETVTRMAEAEVQEGKARKTN 228
y 247 PEVQSTLRKLYLQ 260
b 229 PEIQTSLRKRLYLQ 242
```

RESULT 14

S-10-114-432-28

Sequence 28, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND

FILE REFERENCE: 51158-20066.00

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

S-10-114-432-28

```
Query Match 69.7%; Score 940.5; DB 15; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;
```

```
y 8 MSDFPQLEERYDMSGARLALTLCTVKAREGSEVDMEALERMFRYLKFEFTMKRDPTAQ 67
b 1 MSNPRSLSEEEKYDMSGARLALTLCTVKAREGSEEDLDLEHMFQRLRFESTMKRDPTAE 60
y 68 FLEELDEFQOTIDNWEPSVSCAFVVLMAHGEGLLKGDEKVRLEDLFEVLNNKNCKAL 127
b 61 FQEELEKFAQIDREDPVSCAFVVLMAHGRSGFLKGEDGEMVKLENLFEALNNKNCQAL 120
y 128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPNQSIPTYTDTLHI 186
b 121 RAKPKYIIQACRGEQDPG-----ETVGGDEIYVMWIKDSPTIPTYTDALHV 168
y 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKKGSIIELEETETRLMANTVNMQEGKPRKVN 246
b 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRGHILELLETVTRMAEAEVQEGKARKTN 228
y 247 PEVQSTLRKLYLQ 260
b 229 PEIQTSLRKRLYLQ 242
```

RESULT 15

S-10-114-432-30

Sequence 30, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

GenCore version 5.1.6
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M protein - protein search, using sw model

run on: March 19, 2004, 11:08:15 ; Search time 52.8287 Seconds

(without alignments)
1390.577 Million cell updates/sec

title: US-09-989-903-2

perfect score: 1350

sequence: 1 KPDMESEMDPQLQERYD.....KPRKYNPEVQSTLRKKYLQ 260

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04:*

- 1: geneseq1980s.*
- 2: geneseq1980s.*
- 3: geneseq2000s.*
- 4: geneseq2001s.*
- 5: geneseq2002s.*
- 6: geneseq2003as.*
- 7: geneseq2003bs.*
- 8: geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	281	2	AAW93592 Mouse cas
2	1350	100.0	281	3	AAAY93213 Amino aci
3	1332	98.7	257	3	AAAY68864 Amino aci
4	940.5	69.7	242	3	AAAY93214 Amino aci
5	940.5	69.7	242	5	AAAG77980 Full-leng
6	912.5	67.6	242	5	AAAG77984 Full-leng
7	892.5	66.1	229	3	AAAY68865 Amino aci
8	804.5	59.6	214	3	AAAY93216 Amino aci
9	692.5	51.3	230	3	AAAY93215 Amino aci
10	436	32.3	398	5	ABG76499 DNA encod
11	427	31.6	234	5	AAU72882 Human asp
12	286.5	21.2	261	5	AAU00610 Chimeric
13	276.5	20.5	452	5	ABE10110 Mouse cas
14	276	20.4	277	4	AAU05395 Mouse cas
15	275.5	20.4	435	2	AAU90703 Interleuk
16	274.5	20.3	435	2	AAAG66771 Human int
17	274.5	20.3	435	2	AAAG98462 Human ice
18	274.5	20.3	435	2	AAW26274 Cell deat
19	274.5	20.3	435	2	AAW21716 Amino aci
20	274.5	20.3	435	3	ABE14257 Human ich
21	274.5	20.3	435	4	AAE00599 Human cas
22	274.5	20.3	435	4	ABE78321 Amino aci
23	274.5	20.3	435	5	ABJ01217 Human cas
24	274.5	20.3	435	7	AAE63002 Human pro
25	274.5	20.3	441	2	AAAG6768 Human int

AAE14253 Human ich
ABE79812 Rat caspa
AAE63000 Rat Prote
AAW00372 Apopain C
AAW95831 Human int
AAW00677 Pro-Yama.
AAW41688 Amino aci
AAW47089 Rat inter
AAO19867 Bacteriop
ADD25641 Binding d
AAE63080 Rat Prote
AAW16600 Apopain C
AAV21717 Amino aci
AAU05394 Human cas
AAE63000 Human cas
ABJ01218 Human mem
AAE63082 Human pro
AAE26763 Human cas

ALIGNMENTS

RESULT 1
AAW93592
ID AAW93592 standard; protein; 281 AA.
XX AC AAW93592;
XX AC

DT 21-JUN-1999 (first entry)
DE Mouse caspase-14 protein.
XX

Caspase-14; murine; protease; treatment; apoptotic-related disease;
autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
neurodegenerative disease; ischaemic injury; anti-idiotypic antibody;
caspase-14 processing activity; epitope; competitor; modulator.
XX Mus sp.
XX WO9910504-A2.
XX PD 04-MAR-1999.
XX PF 26-AUG-1998; 98WO-US017715.
XX PR 26-AUG-1997; 97US-0056986P.

(IDUN-) IDUN PHARM INC.
PI Alnemri ES, Fernandes-Alnemri T;
XX WPI; 1999-204670/17.
XX N-PSDB; AAX23515.
XX Newly isolated polynucleotide encoding a caspase-14 polypeptide - useful
for identifying (ant)agonists that are useful in the diagnosis and
treatment of apoptosis-related diseases.
XX Claim 4; Fig 1; 59pp; English.
XX This invention describes a novel murine caspase-14 which has protease
activity. The caspase-14 polypeptide is useful for identifying
(ant)agonists of the polypeptide, where enzyme activity is measured with
a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated
caspase-14 is useful for identifying inhibitors or enhancers of caspase-
14 activity. The compounds identified by both methods form pharmaceutical
compositions for treating apoptotic-related diseases, including
autoimmune disease, cancer, acquired immunodeficiency syndrome (AIDS),
neurodegenerative diseases and ischaemic injury. The anti-caspase-14
antibody is useful for measuring the level of caspase-14 in a tissue

C sample. An antibody that binds to a caspase-14 polypeptide is useful for
 C isolating the polypeptide, and an antibody that binds to the large or
 C small subunit the polypeptide is useful for identifying samples with
 C caspase-14 processing activity. An antibody that binds to caspase-14
 C heterodimer or heterotetramer is useful for isolating caspase-14 with
 C apoptotic activity or in a screening assay to identify antagonists. The
 C antibodies form kits for such purposes. The anti-caspase-14 antibody is
 C also useful for preparing anti-idiotypic antibodies, which mimic a
 C caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,
 C the antibody is useful as a competitor of caspase-14 in reducing the
 C level of caspase-14 activity, which reduces the level of apoptotic
 C activity. Oligonucleotides made from the polynucleotides are useful as
 C polymerase chain reaction (PCR) primers or probes to screen genomic or
 C cDNA libraries for similar caspase-14 encoding polynucleotides, or for
 C diagnosis of diseases associated with enhanced or inhibited apoptosis.
 C The isolated caspase-14 gene permits methods of modulating apoptosis for
 C the treatment of human diseases

X X Sequence 281 AA;

Query Match 100.0%; Score 1350; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 5,7e-130;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 KPDMESESDPQLOERYDMSGARLALTLCVTKAREGEVDMEALRMFYLKPESTMK 60
 b 17 KPDMESESDPQLOERYDMSGARLALTLCVTKAREGEVDMEALRMFYLKPESTMK 76
 Y 61 RDPTAQOFLLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLN 120
 b 77 RDPTAQOFLLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLN 136
 Y 121 NKCKALRGKPKVYIIQACRGEHRDPGELRGNEELGGDEGLGDEAVLKNPQSIPTY 180
 b 137 NKCKALRGKPKVYIIQACRGEHRDPGELRGNEELGGDEGLGDEAVLKNPQSIPTY 196
 Y 181 TDTLHIYSTVEGYLSYRHDKSGFGIQTLDVFIHKKSILELTETRLMANTVWQEG 240
 b 197 TDTLHIYSTVEGYLSYRHDKSGFGIQTLDVFIHKKSILELTETRLMANTVWQEG 256
 Y 241 KPRKNPEVQSTLRKKLYLQ 260
 b 257 KPRKNPEVQSTLRKKLYLQ 276

RESULT 2

AY93213
 ID AAY93213 standard; protein; 281 AA.

AY93213;

04-SEP-2000 (first entry)

Amino acid sequence of a murine caspase-14.

Caspase-14; cell death specific protease; apoptosis stimulator;
 apoptosis; AIDS; neurodegenerative disease; ischemic injury.

Mus sp.

Key Location/Qualifiers
 Region 1..156
 /note= "large subunit"
 Active-site 134..138
 Cleavage-site 156..157
 Cleavage-site 162..163
 Region 163..257
 /note= "small subunit"

WO200028047-A1.

18-MAY-2000.

PF 29-OCT-1999; 99WO-US025523.
 PR 06-NOV-1998; 98US-00187789.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA Alnemri ES, Fernández-Alnemri T;
 XX WPI; 2000-376558/32.
 PI N-PSDB; AAA15163.
 DR Novel nucleic acids encoding cell death specific protease termed caspase-
 XX 14 useful for treating cancers by stimulating apoptosis.

XX Claim 52; Fig 1; 78pp; English.

XX The present sequence represents a murine caspase-14 polypeptide. The
 CC polypeptide is a cell death specific protease, and is an apoptosis
 CC stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
 CC -14 antibodies are useful for treating or reducing the severity of
 CC pathological conditions associated with increased or decreased levels of
 CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
 CC diseases and ischemic injury are treated by administering anti-caspase-14
 CC antibodies. The antibody is useful for determining the presence or the
 CC level of caspase-14 in tissue sample and also for the isolation of
 CC caspase-14 with apoptotic activity or in screening assay to identify an
 CC agent that inhibits heterodimer or heterotetramer formation and
 CC therefore, apoptosis

XX Sequence 281 AA;

Query Match 100.0%; Score 1350; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 5,7e-130;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPDMESESDPQLOERYDMSGARLALTLCVTKAREGEVDMEALRMFYLKPESTMK 60
 Db 17 KPDMESESDPQLOERYDMSGARLALTLCVTKAREGEVDMEALRMFYLKPESTMK 76
 Qy 61 RDPTAQOFLLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLN 120
 Db 77 RDPTAQOFLLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLN 136
 Qy 121 NKCKALRGKPKVYIIQACRGEHRDPGELRGNEELGGDEGLGDEAVLKNPQSIPTY 180
 Db 137 NKCKALRGKPKVYIIQACRGEHRDPGELRGNEELGGDEGLGDEAVLKNPQSIPTY 196
 Qy 181 TDTLHIYSTVEGYLSYRHDKSGFGIQTLDVFIHKKSILELTETRLMANTVWQEG 240
 Db 197 TDTLHIYSTVEGYLSYRHDKSGFGIQTLDVFIHKKSILELTETRLMANTVWQEG 256
 Qy 241 KPRKNPEVQSTLRKKLYLQ 260
 Db 257 KPRKNPEVQSTLRKKLYLQ 276

RESULT 3

AY68864
 ID AAY68864 standard; protein; 257 AA.

AY68864;

16-MAY-2000 (first entry)

Amino acid sequence of a murine caspase-like polypeptide.

Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
 keratinisation; wound healing.

Mus musculus.

WO200004169-A1.

27-JAN-2000.
12-JUL-1999; 99WO-EP004939.
17-JUL-1998; 98EP-00202422.
(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
WPI; 2000-182433/16.
N-PSDB; AAZ60683.
New murine and human caspase homologues useful for treating skin related disorders.
Claim 1; Page 51-52; 68pp; English.
The present sequence represents a murine caspase-like polypeptide. The specification also describes a human caspase-like polypeptide. Caspases are cysteinyl aspartate-specific proteinases which play a central role in apoptosis. The polypeptides of the invention are related to human and murine caspase-2 and human caspase-9, and possess all of the typical amino acids involved in catalysis, including the QACRG box, and contain no or only a very short prodomain. mRNA expression of the homologues of the invention is predominant in the skin. The caspase-like polypeptides are useful for treating human or animal diseases, such as skin diseases. They are also useful for screening for compounds that modulate its activity, i.e. agonists, antagonists, and inhibitors. The caspase-like polypeptides and polynucleotides are useful for modulating keratinisation, for diagnosing and treating inappropriate wound healing

Query Match 98.7%; Score 1332; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.5e-128;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4 MESEMSDQPLQEEYDMSGARLALTLCTVKAREGSEVDMEALERMFLYKPESTMKRDP 63
1 MESEMSDQPLQEEYDMSGARLALTLCTVKAREGSEVDMEALERMFLYKPESTMKRDP 60
64 TAOQFLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLNNKN 123
61 TAOQFLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLNNKN 120
124 CKALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEAVLKNPQSIPTTDT 183
121 CKALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEAVLKNPQSIPTTDT 180
184 LHIYSTVEGYLSYRHDKSGGFQITLTDVFIHKKGSIILEITRLMANTVMOEGKPR 243
181 LHIYSTVEGYLSYRHDKSGGFQITLTDVFIHKKGSIILEITRLMANTVMOEGKPR 240
244 KVNPEVOSTLRKKLYLQ 260
241 KVNPEVOSTLRKKLYLQ 257

RESULT 4
LAY93214
ID AAY93214 standard; protein; 242 AA.
AC AAY93214;
XT 04-SEP-2000 (first entry)
XT Amino acid sequence of a human caspase-14.
CX Caspase-14; cell death specific protease; apoptosis stimulator;
GW apoptosis; AIDS; neurodegenerative disease; ischemic injury.
CX Homo sapiens.
DS

XX Key Location/Qualifiers
FH Region 1. .146
FT /note= "large subunit"
FT Active-site 130. .134
FT Cleavage-site 146. .147
FT Region 147. .242
FT /note= "small subunit"
XX WO200028047-A1.
XX 18-MAY-2000.
XX 29-OCT-1999; 99WO-US025523.
XX 06-NOV-1998; 98US-00187789.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Alnemri ES, Fernandez-Alnemri T;
XX WPI; 2000-376558/32.
XX N-PSDB; AAA15164.
XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
XX Claim 13; Fig 7; 78pp; English.
XX The present sequence represents a human caspase-14 polypeptide. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence or the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an agent that inhibits heterodimer or heterotetramer formation and therefore, apoptosis

Query Match 69.7%; Score 940.5; DB 3; Length 242;
Best Local Similarity 71.3%; Pred. No. 5.9e-88;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;
8 MSDPQLOEERDMSGARLALTLCTVKAREGSEVDMEALERMFLYKPESTMKRDP 67
1 MSNPRLEEEKYDMSGARLALTLCTVKAREGSEVDMEALERMFLYKPESTMKRDP 60
68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLNNKN 127
61 FQEELEKFKQADSDREDPVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLNNKN 120
128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEAVLKNPQSIPTTDT 186
121 RAKPKVYIIQACRGEHRDPGEELRGNEELGGDEAVLKNPQSIPTTDT 168
187 YSTVEGYLSYRHDKSGGFQITLTDVFIHKKGSIILEITRLMANTVMOEGKPR 246
169 YSTVEGYLSYRHDKSGGFQITLTDVFIHKKGSIILEITRLMANTVMOEGKPR 228
247 FVQSTLRKKLYLQ 260
229 FEIQSTLRKKLYLQ 242

RESULT 5
AAG77980
ID AAG77980 standard; protein; 242 AA.
XX

Y 196 YRHDEKSGFIQTLVDVFIHKSGSILELLEETRLMANTENVQEGKPRKVNPEVQSTLRK 255
b 178 YRHDEKSGFIQTLVDVFIHKSGSILELLEETRLMANTENVQEGKPRKVNPEVQSTLRK 237
Y 256 KLYLQ 260
b 238 RLYLQ 242

RESULT 7
AY68865
D AAY68865 standard; protein; 229 AA.
C AAY68865;
X X
T T
E 16-MAY-2000 (first entry)
X Amino acid sequence of a human caspase-like polypeptide.
W Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
W keratinisation; wound healing.
X Homo sapiens.
N WO200004169-A1.
X X
D 27-JAN-2000.
X X
F 12-JUL-1999; 99WO-EP004939.
R X
R 17-JUL-1998; 98EP-00202422.
X (VLAAS) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
X Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
T WPI; 2000-182433/16.
R N-PSDB; AAZ60684.
X New murine and human caspase homologues useful for treating skin related
T disorders.
X Claim 2; Page 53-54; 68pp; English.
X The present sequence represents a human caspase-like polypeptide. The
X specification also describes a murine caspase-like polypeptide. Caspases
X are cysteinyl aspartate-specific proteinases which play a central role in
X apoptosis. The polypeptides of the invention are related to human and
X murine caspase-2 and human caspase-9, and possess all of the typical
X amino acids involved in catalysis, including the QACRG box, and contain
X no or only a very short prodomain. mRNA expression of the homologues of
X the invention is predominant in the skin. The caspase-like polypeptides
X are useful for treating human or animal diseases, such as skin diseases.
X They are also useful for screening for compounds that modulate its
X activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
X polypeptides and polynucleotides are useful for modulating
X keratinisation, for diagnosing and treating inappropriate wound healing

Y 21 MSGARLALTLCTVKAREGSEVDMEALRMFRYLKFBSTMKGRDPTAQOPLLEDFEQTID 80
b 1 MSGARLALTLCTVKAREGSEVDMEALRMFRYLKFBSTMKGRDPTAQOPLLEDFEQTID 60
Y 81 NWEFPVSCAFVVLMAHGEGLLKEGDKVRLLEDLFEVLNNKNCKALRGKPKVYIIQACR 140
b 61 SREFPVSCAFVVLMAHGEGLLKEGDKVRLLEDLFEVLNNKNCKALRGKPKVYIIQACR 120
Y 141 GEHRDPGEELRGNEELGDEBLGDGE-VAVLKNPQSIPTTYTDLHIYSTEVEGILSYRHD 199

Db 121 GQRDPG-----EVGGDEIVWVKDSQIPIYTDALHYSTVEGVIAEHD 168
QY 200 EKGSGFIQTLVDVFIHKSGSILELLEETRLMANTENVQEGKPRKVNPEVQSTLRK 259
Db 169 QKSGCFIQLVDVFTKRGHILELLEETVTRMAEALVQEGKARKTNPEIQTILRKLYL 228
QY 260 Q 260
Db 229 Q 229

RESULT 8
AAY93216
ID AAY93216 standard; protein; 214 AA.
X X
AC AAY93216;
X X
DT 04-SBP-2000 (first entry)
X X
DE Amino acid sequence of a human caspase-14 splice variant.
X X
KW Caspase-14; cell death specific protease; apoptosis stimulator;
KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.
X X
OS Homo sapiens.
X X
FH Key Location/Qualifiers
FT Active-site 102..106
X X
EN WO200028047-A1.
X X
PD 18-MAY-2000.
X X
PF 29-OCT-1999; 99WO-US025523.
X X
PR 06-NOV-1998; 98US-00187789.
X X
XA (UYJE-) UNIV JEFFERSON THOMAS.
X X
PI Alnemri ES, Fernandez-Alnemri T;
X X
DR WPI; 2000-376558/32.
DR N-PSDB; AAA15166.
X X
PT Novel nucleic acids encoding cell death specific protease termed caspase-
PT 14 useful for treating cancers by stimulating apoptosis.
X X
PS Claim 42; Fig 9; 78pp; English.
X X
CC The present sequence represents a human caspase-14 splice variant. The
CC polypeptide is a cell death specific protease, and is an apoptosis
CC stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
CC -14 antibodies are useful for treating or reducing the severity of
CC pathological conditions associated with increased or decreased levels of
CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
CC diseases and ischemic injury are treated by administering anti-caspase-14
CC antibodies. The antibody is useful for determining the presence or the
CC level of caspase-14 in tissue sample and also for the isolation of
CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis
X X
SQ Sequence 214 AA;

Query Match 59.6%; Score 804.5; DB 3; Length 214;
Best Local Similarity 53.0%; Pred. No. 4.7e-74;
Matches 160; Conservative 27; Mismatches 26; Indels 41; Gaps 3;
QY 8 MSQPQLQEBRYDMGSGARLALTLCTVKAREGSEVDMEALRMFRYLKFBSTMKGRDPTAQO 67
Db 1 MSNPSLEEEKYDMGSGARLALTLCTVKAREGSEE----- 34

Y 68 FLEELDEFQOTIDNWEPPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLNNKCKAL 127
 b 35 --EELEKFOQAIIDSRDPVSCAFVVLMAHGREGLKGEDEKVRLEDLFEVLNNKCKAL 92
 Y 128 RGPVKYIIQACRGEHRDPGEELRGNEBELGGDEELGGDE-VAVLKNPQSIPTTDTLHI 186
 b 93 RAKPKYIIQACRGEHRDPGEELRGNEBELGGDEELGGDE-VAVLKNPQSIPTTDTLHI 140
 Y 187 YSTVEGYLSYRDEKSGFIQTLTDFVFIHKKGSILLETETRLMANTENVNQGKPKVN 246
 b 141 YSTVEGYIAYRHDQKSGFIQTLTDFVFIHKKGSILLETETRLMANTENVNQGKPKVN 200
 Y 247 PEVQSTLRKLYLQ 260
 b 201 PEIQSTLRKLYLQ 214

ESULT 9

AY93215
 D AAY93215 standard; protein; 230 AA.

X C AAY93215;

X T 04-SEP-2000 (first entry)

E Amino acid sequence of a human caspase-14 splice variant.

X Caspase-14; cell death specific protease; apoptosis stimulator;
 W apoptosis; AIDS; neurodegenerative disease; ischemic injury.

X S Homo sapiens.

H Key Location/Qualifiers
 T Active-site 130..134

X N WO200028047-A1.

X D 18-MAY-2000.

X F 29-OCT-1999; 99WO-US025523.

X R 06-NOV-1998; 98US-00187789.

X A (UYJE-) UNIV JEFFERSON THOMAS.

X I Alnemri ES, Fernandez-Alnemri T;

X R WPI; 2000-376558/32.

X R N-PSDB; AAA15165.

X T Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.

X S Claim 41; Fig 8; 78pp; English.

X C The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence or the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an agent that inhibits heterodimer or heterotetramer formation and therefore, apoptosis

X Q Sequence 230 AA;

Query Match 51.3%; Score 692.5; DB 3; Length 230;

Best Local Similarity 72.0%; Pred. NO. 1.7e-62;

Matches 134; Conservative 22; Mismatches 17; Indels 13; Gaps 2;

QY 8 MSDPQLQEEERYDMSGARLALTLCVTKAREGSEVDMEALERMERYLKFFSTMKRDPTAQ 67
 Db 1 MSNPSLEEEKYDMSGARLALTLCVTKAREGSEEDLDALEHMERQLRFSTMKRDPTAQ 60
 QY 68 FLEELDEFQOTIDNWEPPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLNNKCKAL 127
 Db 61 FOEELKEFQQAIDSRDPVSCAFVVLMAHGREGLKGEDEKVRLEDLFEVLNNKCKAL 120
 QY 128 RGPVKYIIQACRGEHRDPGEELRGNEBELGGDEELGGDE-VAVLKNPQSIPTTDTLHI 186
 Db 121 RAKPKYIIQACRGEHRDPGEELRGNEBELGGDEELGGDE-VAVLKNPQSIPTTDTLHI 168
 QY 187 YSTVEG 192
 Db 169 YSTVEG 174

RESULT 10

ABG76499

ID ABG76499 standard; protein; 398 AA.

XX AC ABG76499;

XX DT 05-NOV-2002 (first entry)

XX DE DNA encoding protein modification and maintenance molecule #3.

XX KW Protein modification and maintenance molecule; gastrointestinal disorder;
 KW dysphagia; esophageal spasm; gastritis; anorexia; nausea; hypertension;
 KW cardiovascular disorder; atherosclerosis; vasculitis; aneurysm; allergy;
 KW ischaemic heart disease; autoimmune disorder; inflammatory disorder;
 KW acquired immunodeficiency syndrome; AIDS; ankylosing spondylitis; cancer;
 KW anaemia; amyloidosis; cell proliferative; arteriosclerotic bursitis;
 KW cirrhosis; developmental disorder; renal tubular acidosis; anaemia;
 KW bone resorption; epilepsy; epithelial disorder; keratosis; pilaris;
 KW allergic contact dermatitis; insect bite; keloid; dermatofibroma; eczema;
 KW neurological disorder; stroke; cerebral neoplasm; Alzheimer's disease;
 KW Huntington's disease; dementia; reproductive disorder; infertility;
 KW endometriosis; gynecomastia; ectopic pregnancy; gene therapy.

XX OS Homo sapiens.

XX PN WO200260942-A2.

XX PD 08-AUG-2002.

XX 30-JAN-2002; 2002WO-US002813.

XX 31-JAN-2001; 2001US-0265705P.

XX 05-FEB-2001; 2001US-0266762P.

XX 16-FEB-2001; 2001US-0269581P.

XX 23-FEB-2001; 2001US-0271198P.

XX 01-MAR-2001; 2001US-0272813P.

XX 13-MAR-2001; 2001US-0275586P.

XX 23-MAR-2001; 2001US-0278505P.

XX 30-MAR-2001; 2001US-0280533P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Warren BA, Honchell CD, Lu Y, Wallia NK, Burford N, Delegeane AM;
 PI Gandhi AR, Baughn MR, Griffin JA, Gietzen KJ, Lu DAM, Ison CH;
 PI Ramkumar J, Tang TY, Lal PG, Borowski ML, Duggan BM, Hafalia AJA;
 PI Arviru C, Thangavelu K, Yao MG, Elliott VS, Ding L, Yue H, Lee S;
 PI Swarnakar A, Tran UK, Xu Y;

XX DR WPI; 2002-608499/65.

XX DR N-PSDB; ABS58370.

XX PT New protein modification and maintenance molecules useful for treating or
 PT preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
 PT cell proliferative, developmental, neurological and reproductive
 PT disorders.

XX Claim 1; Page 133-134; 172pp; English.

XX The invention describes an isolated human polypeptide (I), a naturally occurring amino acid sequence at least 90 % identical to the protein, or a biologically active fragment or an immunogenic fragment of the protein. The protein modification and maintenance molecules are useful in the diagnosis, treatment, and prevention of gastrointestinal (e.g. dysphagia, esophageal spasm, gastritis, anorexia or nausea), cardiovascular (e.g. atherosclerosis, hypertension, vasculitis, aneurysms, or ischaemic heart disease), autoimmune/inflammatory (e.g. acquired immunodeficiency syndrome (AIDS), allergies, ankylosing spondylitis, anaemia or amyloidosis), cell proliferative (e.g. cancers, arteriosclerotic, bursitis, or cirrhosis), developmental (e.g. renal tubular acidosis, anaemia, bone resorption, or epilepsy), epithelial (e.g. allergic contact dermatitis, keratosis pilaris, insect bites, keloid, dermatofibroma or eczema), neurological (e.g. stroke, cerebral neoplasms, Alzheimer's disease, Huntington's disease or dementia), and reproductive disorders (e.g. infertility, endometriosis, gynaecomastia or ectopic pregnancy). These may also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of protein modification and maintenance molecules. Polynucleotides are useful in somatic and germline gene therapy. This is the amino acid sequence of a protein modification and maintenance molecule described in the invention

XX Sequence 398 AA;

Query Match 32.3%; Score 436; DB 5; Length 398;
Best Local Similarity 33.2%; Pred. No. 9.4e-36;
Matches 104; Conservative 46; Mismatches 77; Indels 38; Gaps 7;

2Y 10 DPQLQEYDMSGARLALTLCVTKAREGSEVDMEALERFVRLKFESTMKRDPPTAQQL 69
b 157 EPACSTQYDLSKARALLAVIQGRPGAGHDVEALGGLCWALGHFTVTRDPTAQAFQ 216
2Y 70 EELDEFQOTIDNWEPEVSCAFVILMAH-GEGLLKGEDEKXVLEDLFVILNNKNCALR 128
b 217 EELAQFQELDTCRGPVSCALVALMAHGGPRGQLLGADGQEVQPEALMQELS--RCQVLIQ 274
2Y 129 GKPKVYIIOACGSEHRDPG-----BELRGNEELGDEELGGDEVAVLKNPQSP 178
b 275 GRPKIFLQACRGNRDAGVGFTALPWTWSWLR-----PFSVP 313
2Y 179 TYTDTLHYSTVEGYLSYRHDKSGGFIQTLDYFIHKG-SILELTFEITRLMANTEVM 237
b 314 SHADVLIQIYAEAGGVAYR-DDKGSDFIQTLEVLNRPANPGRLLELLTEVNRVCEVL 372
2Y 238 QE--GKPKVNPVQSTLRKLYIQ 260
b 373 GPDCELEKACLEIRSSLRRLCLQ 397

RESULT 11
AAU72882
ID AAU72882 standard; protein; 234 AA.
XX AAU72882;
XX AAU72882;
DT 26-FEB-2002 (first entry)
DE Human aspartyl protease partial protein sequence #7.
XX Human; protease; PCR primer; cytostatic; immunomodulator; cardiac; vasotropic; antimigraine; analgesic; endocrine; nocotropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic; anorectic; antiinflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoietic; breast; colon; lung; prostate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; dyskinesia; metabolic disorder; inflammatory disorder.

OS Homo sapiens.
XX WO200183782-A2.
XX 08-NOV-2001.
XX 04-MAY-2001; 2001WO-US014431.
XX 04-MAY-2000; 2000US-0201879P.
XX (SUGE-) SUGEN INC.
XX Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S; Payne V;
XX WPI; 2002-041502/05.
XX N-PSDB; AAS97165.
XX Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraines, pain, psychotic and inflammatory disorders.
XX Claim 28; Fig 2A; 232pp; English.
XX The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoietic origin, of the breast, colon, lung, prostate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g. central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAU72876-AAU72910 represent human protease amino acid sequences of the invention

XX Sequence 234 AA;

Query Match 31.8%; Score 427; DB 5; Length 234;
Best Local Similarity 39.7%; Pred. No. 3.6e-35;
Matches 102; Conservative 45; Mismatches 72; Indels 38; Gaps 7;

QY 18 RYDMSGARLALTLCVTKAREGSEVDMEALERFVRLKFESTMKRDPPTAQQLLELDEFQ 77
b 1 QYDLSKARALLAVIQGRPGAGHDVEALGGLCWALGHFTVTRDPTAQAFQELAQFRE 60
QY 78 TIDNWEPEVSCAFVILMAH-GEGLLKGEDEKXVLEDLFVILNNKNCALGKPKVYII 136
b 61 QLDTCRGPVSCALVALMAHGGPRGQLLGADGQEVQPEALMQELS--RCQVLOGRPKIFLL 118
QY 137 QACGSEHRDPG-----BELRGNEELGDEELGGDEVAVLKNPQSPITYTDTLHI 186
b 119 QACRGNRDAGVGFTALPWTWSWLR-----PFSVSHADVIQI 157
QY 187 YSTVEGYLSYRHDKSGGFIQTLDYFIHKG-SILELTFEITRLMANTEVMQE--GKPR 243
b 158 YAEAGGVAYR-DDKGSDFIQTLEVLNRPANPGRLLELLTEVNRVCEQVLGPDCELR 216
QY 244 KNPVQSTLRKLYIQ 260
b 217 KACLEIRSSLRRLCLQ 233

RESULT 12
AAE00610
ID AAE00610 standard; protein; 261 AA.
XX AAE00610;
XX

T 02-JUL-2001 (first entry)
X Chimeric cassette comprising human caspase with modified cleavage site.
X Human; caspase; beta-secretase; cleavage site; interdomain linker;
W cysteine protease; apoptosis; caspase expression cassette; metastasis;
W tumour; cathepsin B; urokinase; proliferation; gene therapy; chimera;
W Alzheimer's disease.
S Homo sapiens.
S Unidentified.
S Chimeric.
H Key
I Location/Qualifiers
I Region 1..147
I /label= Caspase_large_subunit
I /note= "Beta-secretase cleavage site which replaces the
I naturally occurring caspase cleavage site"
I 166..261
I /label= Caspase_small_subunit
T WO200129232-A2.
N 26-APR-2001.
X 19-OCT-2000; 2000WO-US028941.
X 20-OCT-1999; 99US-0160559P.
R 14-AUG-2000; 2000US-0225564P.
R (SCIO-) SCTOS INC.
A Cordell B, Li Y;
I WPI; 2001-290920/30.
R N-PSDB; AAD03918.
R Novel fusion polypeptide comprising first and second caspase subunit
T separated by cleavage site not associated in nature with caspase subunit,
T useful for cloning gene encoding enzymes involved in proteolytic
T cleavage.
X Example 1; Fig 27; 116pp; English.
S The present amino acid sequence is an artificially engineered chimeric
S cassette construct comprising human caspase-3 with interdomain linker
C replaced by a Swedish mutant beta-secretase cleavage site. This modified
C caspase-3 plays a pivotal role in Alzheimer's disease. Caspases are a
C family of cysteine proteases, that participate in the initiation and
C execution of apoptosis. Caspases exist as pro-enzymes, activated by
C cleavage into a large and small subunit, occurring after specific
C aspartic acid residues within the pro-enzyme sequence. The present
C invention relates to a method for functional cloning of genes encoding
C proteins or enzymes involved in proteolytic cleavage. The invention is
C based on the use of caspase expression cassettes comprising the coding
C sequence of a proteolytic cleavage site flanked by sequences encoding two
C caspase subunits. A fusion polypeptide comprising a first and a second
C caspase subunit, separated by a cleavage site not associated in nature,
C is useful for cloning gene encoding enzymes involved in proteolytic
C cleavage. An expression cassette containing fusion polypeptide is used to
C identify a mutant cell line deficient in an enzyme of interest and is
C also useful for diagnosis and suppression of proliferation or metastases
C of a tumour cell characterised by overexpression of a polypeptide (e.g.
C Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA
C encoding fusion polypeptide is used in gene therapy
X Sequence 261 AA;
X Query Match 21.2%; Score 286.5; DB 4; Length 261;
X Best Local Similarity 32.1%; Pred. No. 1.2e-20;
X Matches 85; Conservative 41; Mismatches 104; Indels 35; Gaps 9;

QY 16 BERYDMGARGALALTLCTVK-----AREGSEYDMEALERMFRYLKFESTMKRDPTA 65
DB 7 DNSYKMDYPEMGLCIIINNNKFNHKSCTGWTSGTVDVDAANLRETFNKLKYEVRNKNDLFR 66
QY 66 QQFLELDEFOOTIDNWEBPVSCAFV-VLMAHGEGLKGEDEKMYRLDELFEVLNNKC 124
DB 67 ----BEIVELMRDYSKEDHKSRSFVCLLSHGEEGIIFGTNGP-VDLKKITNFFRGDRC 121
QY 125 KALRGKPKVYIIQACRGEHRDPGEELRGNE--BLGGDEELGGDEVAVLKNNPQSIPTYTD 182
DB 122 RSLGCKPKLFIQACRGTGELDCGIEETKTEISEVNLDAEPFHDMSACHK-----IPVEAD 176
QY 183 TIHYSTVEGYLSYRDEKSGFIQILTVFIHKKSILELITEITRLMANTVEMOEGK- 241
DB 177 FLYAYSTAPGYISWRNSKDGSWFIQSLC-AMLKQYADKLEFHMILTRV--NRKVATEFES 233
QY 242 -----PRKVNPEVOSTLRKKLY 258
DB 234 PSFATFHAQKQIFCIIVSMLTKEYL 258
RESULT 13
ABB10110
ID ABB10110 standard; protein; 452 AA.
XX AC ABB10110;
XX AC ABB10110;
DT 26-JUL-2002 (first entry)
DE Mouse caspase 2 protein.
XX KW Caspase 2; antisense; cytostatic; osteopathic; cerebroprotective;
KW neuroprotective; antilipemic; antiinflammatory; antimicrobial;
KW haematopoietic disorder; bone metabolism disorder; cholesterol disorder;
KW hyperproliferative disorder; cancer; blood disorders; stroke;
KW brain injury; neurodegenerative disease; infection; inflammation; tumour.
XX OS Mus musculus.
XX PN WO200224720-A1.
XX XX 28-MAR-2002.
XX PF 14-SEP-2001; 2001WO-US028631.
XX PR 20-SEP-2000; 2000US-00667018.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Zhang H, Watt AT;
XX DR WPI; 2002-351998/38.
XX DR N-PSDB; ABB58563.
XX PT New antisense compounds targeted to nucleic acid molecule encoding
PT caspase 2, useful for treating diseases or conditions associated with
PT caspase 2, e.g. cancer, blood disorders, stroke, brain injury and
PT neurodegenerative diseases.
XX Example 13; Page 111-113; 146pp; English.
XX The invention relates to a compound 8-50 nucleobases in length targeted
CC to a nucleic acid molecule encoding caspase 2 which specifically
CC hybridises with and inhibits the expression of caspase 2, or specifically
CC hybridises with at least an 8-nucleobase portion of an active site on a
CC nucleic acid molecule encoding caspase 2. The activity of antisense
CC oligonucleotides of the invention may be described as, cytostatic,
CC osteopathic, cerebroprotective, neuroprotective, antilipemic,
CC antiinflammatory and antimicrobial. The antisense compounds are useful
CC for treating an animal having a disease or condition associated with
CC caspase 2, such as haematopoietic disorder, bone metabolism disorder,
CC cholesterol disorder, or a hyperproliferative disorder. These compounds
CC may further be used as research reagents and diagnostics, to distinguish

IC between functions of various members of a biological pathway, in the
IC treatment of a disease or disorder which can be treated by modulating the
IC expression of caspase 2, including cancer, blood disorders, stroke, brain
IC injury and neurodegenerative diseases. They may also be used for
IC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
IC formation. The current sequence represents the mouse caspase 2 protein
XQ Sequence 452 AA;

Query Match 20.5%; Score 276.5; DB 5; Length 452;
Best Local Similarity 30.6%; Pred. No. 2.9e-19;
Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;
Y 36 REGSEVMEALERFRYLKPESTMKDPTAQOFLBELDEFQOTIDNWEFVSCAFVILMA 95
b 219 RSGGDVHTTLVTLFKLGVNVHLVDQTAQEMQKLFQAFQ-LPAHRVTDSCV-VALLS 276
Y 96 HGEGLLKGEDEKXVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHDPG---EELRG 152
b 277 HGVEGGIYGVGKLLQQLQVFRUFDNANCPSONKPMFFIQACRGEHDPGQDQGN 336
Y 153 NEELGGDEELGGDEVAVLKNNPQSIPTYTDTLHIYSTVEGYLSYRHKDGGSGFIQTLTDV 212
b 337 HTQSPGCEESDAGKELMK--NRLPTRSDMIGYACLKGNAMRNTKSGSNYIEALTQV 393
Y 213 FIIHKGS--ILELTEETRLMANTVMOEGK---RKVNPEVQSTLRKKLYL 259
b 394 FSERACDMHVADMLVKVNALIKERGVAPGTPEFRCKEMSEYCVSTLCQQLYL 445

RESULT 14

LAU05395
ID AAU05395 standard; protein; 277 AA.

AC AAU05395;

DT 24-OCT-2001 (first entry)

DE Mouse caspase 3.

GW Mouse; caspase 3; apoptosis; hyperproliferative disorder; hepatitis;
GW viral infection; haematopoietic disorder; autoimmune disorder;
GW atherosclerosis; neurological disorder.

XS Mus musculus.

XN WO200153310-A1.

PD 26-JUL-2001.

PF 11-JAN-2001; 2001WO-US000888.

PR 18-JAN-2000; 2000US-00484617.

PA (ISIS-) ISIS PHARM INC.

PI Zhang H, Cowsett LM;

DR WPI; 2001-442252/47.

DR N-PSDB; AAS10510.

PT New antisense compound to inhibit caspase 3 is useful for treating

PT hepatitis and atherosclerosis.

PS Disclosure; Page 96-97; 127pp; English.

CC The present sequence representing mouse caspase 3 is described in an
CC invention relating to novel antisense oligonucleotides (AAS10517-
CC AAS10876) and methods of using these compounds for the modulation of
CC caspase 3 expression. The caspase 3 antisense oligonucleotides
CC specifically hybridise with and inhibit the expression of caspase 3.
CC Antisense compounds targeted to caspase 3 are useful to inhibit caspase 3
CC expression in cells or tissues and to modulate apoptosis. The caspase 3

CC antisense oligonucleotides are useful for treating disorders associated
CC with expression of caspase 3. Such disorders include hyperproliferative
CC disorders (e.g. cancer), viral infections (e.g. hepatitis),
CC haematopoietic disorders, autoimmune disorders, atherosclerosis and
CC neurological disorders (e.g. Alzheimer's disease)

XQ Sequence 277 AA;

Query Match 20.4%; Score 276; DB 4; Length 277;
Best Local Similarity 33.3%; Pred. No. 1.5e-19;
Matches 79; Conservative 39; Mismatches 81; Indels 38; Gaps 9;
QY 35 AREGSVDMEALERFRYLKPESTMKDPTAQOFLBELDEFQOTIDNWEFVSCAFV-VL 93
b 63 SRSGTDVAANLRFTFMGLKYQVRNKNLDTREDILELMD----SVSKEDSKRSFVCVI 118
QY 94 MAHGEGLLKGEDEKXVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHDPGCELGRN 153
b 119 LSHGDEVIYGTNGP-VELKLTSPFRGDYCSLTGKPKLFIQACRGTLEDCCIE---- 173
QY 154 BELGGDEELGGDEVAVLKNNPQSIPTYTDTLHIYSTVEGYLSYRHKDGGSGFIQTLTD-- 211
b 174 TDSGTDEEMA-----CQKIPVEADFLYASTAPGYYSWRNSKDGSWFIQSLCSML 223
QY 212 -VFIHKGSILTEETRLMANTVMOEGK-----PRKVNPEVQSTLRKKLY 258
b 224 KLYAHR-----LEFMIILTRV--NRKVATEFESFLDSTFHAKKQIPICIVSMLTRELY 274

RESULT 15

AAR90703
ID AAR90703 standard; protein; 435 AA.

AC AAR90703;

DT 10-APR-1996 (first entry)

DE Interleukin-1-beta converting enzyme like apoptosis protease-2.

XW Interleukin-1-beta converting enzyme like apoptosis protease-2;
XW ICE-LAP-2; cell death; immunosuppression; AIDS; Alzheimer disease;
XW Parkinson disease; septic shock; rheumatoid arthritis; head injury;
XW antitumour; antiviral.

OS Homo sapiens.

PN WO9600297-A1.

XX 04-JAN-1996.

XX 23-JUN-1994; 94WO-US007127.

XX 23-JUN-1994; 94WO-US007127.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Wei WH, Craig AR, Hastings GA, Hudson PL, Kirkness EF;

XX WPI; 1996-068881/07.

XX N-PSDB; AAT15579.

PT Interleukin-1 beta converting enzyme like apoptosis protease-1 and -2 -
PT controls programmed cell death, used in treatment of immunosuppression
PT related disorders, e.g. AIDS and Alzheimer's disease.

PS Claim 1; Fig 2A-C; 58pp; English.

CC Human interleukin-1-beta converting enzyme like apoptosis protease-2 (ICE
CC LAP-2) (AAR90703) is structurally related interleukin-1-beta converting
CC enzyme, which is responsible for apoptosis. Recombinant ICE-LAP-2 is
CC obtd. by expression of encoding cDNA (AAT15579) in procaryotic or
CC eucaryotic host cells. It is used to treat diseases related to abnormally
CC controlled programmed cell death, to control vertebrate development and

c tissue homeostasis, to overcome viral infections and to treat
c immunosuppression-related disorders

x
2 Sequence 435 AA;
Query Match 20.4%; Score 275.5; DB 2; Length 435;
Best Local Similarity 29.6%; Pred. No. 3.4e-19;
Matches 68; Conservative 53; Mismatches 100; Indels 9; Gaps 4;
y 36 RGSSEYDMEALSRMRYLKPFSTMRKDPDPAQFLBELDEFQQTIDNWEPPVSCAFVVLMA 95
b 202 RGGDVHDHSTLTFLKLLGYDVHVLCDQTAGEMQEKLQNFQA-LPAHRVTDSC-IVALLS 259
y 96 HGEGLLKGEDEKXVRLEDLFEVLANNKCKALRGPKVYIIQACRGHRDPGEELRGNEE 155
b 260 HGVEGAIYGVGKLLQLQEVFQDFNANCPSLQNKPKMFFIQCACRGDETRGVDDQDGKN 319
y 156 LGGDEBLGGDEVAVLKNPFQSIPTVTDTHIYSTVEGYLSYRHDKSGSGFTQTLTDVFIH 215
b 320 HAGSPGCEBSDAGKEKLPKORLPTRSDMICGYACUKGTAAWRNTKRGSWYIEALAQVF-S 378
y 216 KKGSIILELTFEITRLMANTENVMQGKPR-----KVNPEVQSTLRKKLYL 259
b 379 ERGCDMHVADMLVKVNAIKDREGVAPGTEPHRCCKEMSEYCGSTLCRHLYL 428

earch completed: March 19, 2004, 11:22:14
ob time : 55.8287 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 19, 2004, 11:17:55 ; Search time 34.7092 Seconds
(without alignments)

2199.863 Million cell updates/sec

Title: US-09-989-903-5

Perfect score: 1239

Sequence: 1 MSNPRSLSEKDYMSGAALA.....KARKTNPEIQSTLRKELYIQ 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum Match 100%

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	24.1	452	11 Q8C9H7	Q8C9H7 mus musculus
2	295	23.8	452	11 Q8K241	Q8K241 mus musculus
3	293	23.6	452	11 Q55194	Q55194 rattus norv
4	289.5	23.4	423	13 Q91B67	Q91B67 xenopus lae
5	289	23.3	435	4 Q95UP7	Q95UP7 homo sapien
6	284.5	23.0	283	13 Q91A17	Q91A17 gallus gall
7	279.5	22.6	316	5 Q817B0	Q817B0 geodia cydo
8	279.5	22.6	426	5 Q816Y2	Q816Y2 geodia cydo
9	275.5	22.2	277	6 Q8MJC3	Q8MJC3 cryptolagus
10	275.5	22.2	277	6 Q8MJC1	Q8MJC1 felis silve
11	274.5	22.2	277	6 Q95ND5	Q95ND5 sus scrofa
12	274.5	22.2	383	13 Q919L7	Q919L7 brachydanio
13	273.5	22.1	313	11 Q8CHV5	Q8CHV5 mus musculus
14	272.5	22.0	277	6 Q8MK15	Q8MK15 canis fami
15	272	22.0	399	13 Q91B63	Q91B63 xenopus lae
16	270	21.8	303	11 Q88550	Q88550 rattus norv

Q9R0T0 mus musculu
Q90WU1 gallus gall
Q98UI8 brachydanio
Q81B8 oryzias lat
Q83Q0 mus musculu
Q8C3Q9 mus musculu
Q86FL0 anopheles s
Q90WU0 gallus gall
Q91B63 brachydanio
Q91B64 xenopus lae
Q91B62 xenopus lae
Q9YIU6 pristionchu
Q9JHK1 rattus norv
Q8JGM9 figu rubrip
Q91B65 xenopus lae
Q8JG42 figu rubrip
Q8IUP5 homo sapien
Q8BNT4 mus musculu
Q94089 mus musculu
Q8JIS9 oryzias lat
Q99M47 mus musculu
Q819V7 bombyx mori
Q81955 spodoptera
Q77623 ovis aries
Q35397 rattus norv
Q81TP3 brachiosco
Q9JHX4 rattus norv
Q9GV89 hydra atten
Q9DDJ2 brachydanio

ALIGNMENTS

RESULT 1

ID	Q8C9H7	PRELIMINARY;	PRT;	452 AA.
AC	Q8C9H7;			
DT	01-MAR-2003 (TRENBLrel. 23, Created)			
DT	01-MAR-2003 (TRENBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)			
DE	Caspase 2.			
GN	CASP2.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Thymus;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002).			
DR	EMBL; AK042072; BAC31153.1; ..			
DR	MGD; MGI:97295; Casp2.			
DR	GO; GO:0005632; C:intracellular; IEA.			
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.			
DR	GO; GO:0030693; F:caspase activity; IEA.			
DR	GO; GO:0006915; P:apoptosis; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR001315; CARD.			
DR	InterPro; IPR001309; ICE D20.			
DR	InterPro; IPR002138; ICE P10.			
DR	InterPro; IPR002398; Peptidase_C14.			
DR	Pfam; PF00619; CARD; 1.			
DR	Pfam; PF08656; Peptidase_C14; 1.			
DR	PRINTS; PR00376; ILIBCNZYME.			
DR	SMART; SM00114; CARD; 1.			
DR	SMART; SM00115; CASC; 1.			
DR	PROSITE; PS50209; CARD; 1.			


```
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS50207; CASPASE_P10; 1.
R PROSITE; PS50208; CASPASE_P20; 1.
Q SEQUENCE 452 AA; 50689 MW; C3715908508619CA CRC64;

Query Match 24.1%; Score 298; DB 11; Length 452;
Best Local Similarity 31.9%; Pred. No. 5.8e-17;
Matches 76; Conservative 51; Mismatches 75; Indels 36; Gaps 7;

Y 29 REGSEEDLDALEHMFRLQFESTMKRDPDTAEQFOBELEKFOQAIQDSREDPVSCAFVILMA 88
b 219 RSGGDVDHTTLVTLFLKLGYNVHVLHDQTAQEMQKLNQFAQ-LPAHRVTDSCV-VALLS 276

Y 89 HGREGLKGEDGEMVKLENLFEALNNKNQALRAKPKVYIIQACRGGEQDPG----- 140
b 277 HGVEGGIYGVGKLLQLOEVFLFDNANCPSLQNKPKWFFIQACRGDETGRGVDDQDGKN 336

Y 141 -----ETVGGDEIVMWIKDSPQTIPTVDALHYVSTVEGYIAYRHDKGSCFIQTLV 192
b 337 HTQSPGCEESDAGKEELMKR-----LPTSDMICGYACILKGNAAMRNTRKGSWYIEALT 391

Y 193 DVFTKR--KGHILELLTEVTRMAEAELVOEGKARKTN-----PEIQSTLRKRLYL 241
b 392 QVFSERACDMHADMVLKVNALIKE-----REGYAPGTFFHRCKEMSEYCSILCQQLYL 445

Y 89 HGREGLKGEDGEMVKLENLFEALNNKNQALRAKPKVYIIQACRGGEQDPG----- 140
b 277 HGVEGGIYGVGKLLQLOEVFLFDNANCPSLQNKPKWFFIQACRGDETGRGVDDQDGKN 336

Y 141 -----ETVGGDEIVMWIKDSPQTIPTVDALHYVSTVEGYIAYRHDKGSCFIQTLV 192
b 337 HTQSPGCEESDAGKEELMKR-----LPTSDMICGYACILKGNAAMRNTRKGSWYIEALT 391

Y 193 DVFTKR--KGHILELLTEVTRMAEAELVOEGKARKTN-----PEIQSTLRKRLYL 241
b 392 QVFSERACDMHADMVLKVNALIKE-----REGYAPGTFFHRCKEMSEYCSILCQQLYL 445

RESULT 2
8K241 D Q8K241 PRELIMINARY; PRT; 452 AA.
C Q8K241
T 01-OCT-2002 (TREMELrel. 22, Created)
T 01-OCT-2002 (TREMELrel. 22, Last sequence update)
T 01-OCT-2003 (TREMELrel. 25, Last annotation update)
E Caspase 2.
N CASP2.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
N [1]
P SEQUENCE FROM N.A.
A Strausberg R.;
L Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
R EMBL; BC034262; AAH34262.1; -.
R MGD; MGI197295; Casp2.
R GO; GO:0005622; C:intracellular; IEA.
R GO; GO:0016329; F:apoptosis regulator activity; IEA.
R GO; GO:0030693; F:caspase activity; IEA.
R GO; GO:0006915; P:apoptosis; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR001315; CARD.
R InterPro; IPR002138; ICE_P10.
R InterPro; IPR001309; ICE_P20.
R InterPro; IPR002398; Peptidase_C14.
R Pfam; PF00619; CARD; 1.
R PRINTS; PR00376; ILIBENZYM.
R SMART; SM00114; CARD; 1.
R SMART; SM00115; CASC; 1.
R PROSITE; PS50209; CARD; 1.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS50207; CASPASE_P10; 1.
R PROSITE; PS50208; CASPASE_P20; 1.
Q SEQUENCE 452 AA; 50661 MW; A4DB25A712FAB855 CRC64;

Query Match 23.8%; Score 295; DB 11; Length 452;
Best Local Similarity 31.5%; Pred. No. 1e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Y 29 REGSEEDLDALEHMFRLQFESTMKRDPDTAEQFOBELEKFOQAIQDSREDPVSCAFVILMA 88
b 219 RSGGDVDHTTLVTLFLKLGYNVHVLHDQTAQEMQKLNQFAQ-LPAHRVTDSCV-VALLS 276

Y 89 HGREGLKGEDGEMVKLENLFEALNNKNQALRAKPKVYIIQACRGGEQDPG----- 140
b 277 HGVEGGIYGVGKLLQLOEVFLFDNANCPSLQNKPKWFFIQACRGDETGRGVDDQDGKN 336

Y 141 -----ETVGGDEIVMWIKDSPQTIPTVDALHYVSTVEGYIAYRHDKGSCFIQTLV 192
b 337 HTQSPGCEESDAGKEELMKR-----LPTSDMICGYACILKGNAAMRNTRKGSWYIEALT 391

Y 193 DVFTKR--KGHILELLTEVTRMAEAELVOEGKARKTN-----PEIQSTLRKRLYL 241
b 392 QVFSERACDMHADMVLKVNALIKE-----REGYAPGTFFHRCKEMSEYCSILCQQLYL 445

RESULT 3
O55194 D O55194 PRELIMINARY; PRT; 452 AA.
AC O55194
DT 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE NEDD2/ICH-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98087427; PubMed=9427555;
RA Sato N., Milligan C.E., Uchiyama Y., Oppenheim R.W.;
RT "Cloning and expression of the cDNA encoding rat caspase-2.";
RL Gene 202:127-132(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA Jin K.L., Simon R.P., Graham S.H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U77933; AA896379.1; -.
DR EMBL; AF138231; AAD33684.1; -.
DR PIR; JC8507; JC6507.
DR HSSP; P29466; LICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
Q SEQUENCE 452 AA; 50728 MW; 03F9D096B741CE3 CRC64;

Query Match 23.6%; Score 293; DB 11; Length 452;
Best Local Similarity 31.5%; Pred. No. 1.5e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Y 29 REGSEEDLDALEHMFRLQFESTMKRDPDTAEQFOBELEKFOQAIQDSREDPVSCAFVILMA 88
b 219 RSGGDVDHTTLVTLFLKLGYNVHVLHDQTAQEMQKLNQFAQ-LPAHRVTDSCV-VALLS 276

Y 89 HGREGLKGEDGEMVKLENLFEALNNKNQALRAKPKVYIIQACRGGEQDPG----- 140
b 277 HGVEGGIYGVGKLLQLOEVFLFDNANCPSLQNKPKWFFIQACRGDETGRGVDDQDGKN 336

Y 141 -----ETVGGDEIVMWIKDSPQTIPTVDALHYVSTVEGYIAYRHDKGSCFIQTLV 192
b 337 HTQSPGCEESDAGKEELMKR-----LPTSDMICGYACILKGNAAMRNTRKGSWYIEALT 391

Y 193 DVFTKR--KGHILELLTEVTRMAEAELVOEGKARKTN-----PEIQSTLRKRLYL 241
b 392 QVFSERACDMHADMVLKVNALIKE-----REGYAPGTFFHRCKEMSEYCSILCQQLYL 445
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b 320 HAGSPCESDSAGK-----KLPKMLPFRSMICGYACLGKTAARVTKGSGWYIALA 374
y 193 DVFTKR--KGHILELLETVTRMAEAEVQEGKARTN-----PEIQSTLRKRLYL 241
b 375 QVFSERACDMHADMVAKVNALIKD-----REGYAPGTBFHRCKEMSEYCSLCHRLYL 428

RESULT 6
93417 D O93417 PRELIMINARY; PRT; 283 AA.
C O93417;
T 01-NOV-1998 (TrEMBLrel. 08, Created)
T 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E Caspase-3
S Gallus gallus (Chicken).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
C Gallus.
X NCBI_TaxID=9031;
N [1]
P SEQUENCE FROM N.A.
X MEDLINE=20149872; PubMed=10684799;
A Johnson A.L., Bridgman J.T.;
T "Caspase-3 and -6 expression and enzyme activity in hen granulosa
  cells.";
L Biol. Reprod. 62:589-598(2000).
R EMBL; AF083029; AAC32602.1; -.
R HSP; P42574; IPAU.
R MEROPS; C14.003; -.
R GO; GO:0030693; F:caspase activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR002138; ICE_P10.
R InterPro; IPR001309; ICE_P20.
R Pfam; PF00656; Peptidase_C14.
R PRINTS; PR00376; ILIBENZYM.
R SMART; SM00115; CASG; 1.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS0207; CASPASE_P10; 1.
R PROSITE; PS0208; CASPASE_P20; 1.
Q SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 23.0%; Score 284.5; DB 13; Length 283;
Best Local Similarity 30.3%; Pred. No. 4.6e-16;
Matches 76; Conservative 47; Mismatches 101; Indels 27; Gaps 7;

y 7 LEBEKYDMSGAALALILCVT-----KAREGSEEDLDALEHMFRLPQRFESTMKRDP 56
b 40 LPDDSYRMDYPEIGVCVVIINKNFHRDTGLSSKSGTDADAASVREVMKLGKVKLNNDL 99
y 57 TAEQFQBELEKFOAIDSRDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKN 116
b 100 SSRDIFKLLKNVSEEDHRSKSSPVC---VLLSGDGLFYGTGDL-ELKVITSLFPGDK 155
y 117 COALRAKPKYIIQACRGEQDPG--ETVGGSEIVNVKDSPTIPTYTDALHVVYSTVEG 174
b 156 CRSLAGKFLFFIQACRGTGLDSIEADSPDETVC-----QKIPVEADFLYAYSTAPG 209
y 175 YIAYRHQKSCITQILVDVFTK--RKGHILELLETVTRMAEAEV---QEGKARTNP 229
b 210 YGWRNAEAGSWFIQSLCRLMKHARKLELMQLTRVNRRAVEYSCSTQDFNAKKQIP 269
y 230 EIQSTLRKRLYL 240
b 270 CIVSMLTKEFY 280

RESULT 7
817B0 PRELIMINARY; PRT; 316 AA.
D Q817B0
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AC Q817B0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RT Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RA "Caspase-mediated apoptosis in sponges: cloning and function.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ417903; CAD10676.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
SQ SEQUENCE 316 AA; 35319 MW; 33A46BCCB6C3F9B7 CRC64;

Query Match 22.6%; Score 279.5; DB 5; Length 316;
Best Local Similarity 28.2%; Pred. No. 1.4e-15;
Matches 78; Conservative 54; Mismatches 94; Indels 51; Gaps 9;

Qy 9 EBYKMSG--AALAIL-----CVTKAREGSEEDLDALEHMFRLPQRFESTMKRDP 60
Db 37 KDAYKMSRPRGMALINNRNFTCGMKERVCTDKAENLYGLFNWGLMATIRKDNLTGKA 96
Qy 61 FQBELEKFOAIDSRDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNQAL 120
Db 97 MTRFEDLARHDSAYD---CVVAILTHGISGLYSTGDLIFVEDLTXYFDGVNRP 153
Qy 121 RAKPKYIIQACRGEQDPG---ETVGG-----DEIVNVKDSPT- 158
Db 154 ICKPKYVYVQACRGGKFDYGVSESESTDGESGVNKETANEMMERQFDKWEKALDADETD 213
Qy 159 -----IPTVTDALHVVYSTVEGVIAVRHDKQKSCITQILVDVF--TKRGHILELITE 208
Db 214 GGYSEALPTADFLYAYVPGVSVNSENSEYSGWFIKAFVDTWRDLASKEHFNDILTE 273
Qy 209 VTRMAEAEVQEGKARTNPFIQ---STLRKRLYLQ 242
Db 274 VNRKVA-----YDFQSGRGNKQIPAPVTMLTRKLYFR 305

RESULT 8
Q816Y2 PRELIMINARY; PRT; 426 AA.
AC Q816Y2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
GN CASP-3L.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Eukaryota;
RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
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EMBL; AJ344144; CAC83013.1; -
GO; GO:0030693; F:caspace activity; IEA.
InterPro; IPR00138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PF00656; Peptidase C14.
PRINTS; PR00376; ILIBCNZYME.
SMART; SM00115; CASc; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
SEQUENCE 426 AA; 48024 MW; 713BEEC82BED0C1 CRC64;
Query Match 22.6%; Score 279.5; DB 5; Length 426;
Best Local Similarity 28.2%; Pred. No. 2e-15;
Matches 78; Conservative 54; Mismatches 94; Indels 51; Gaps 9;
2Y 9 EKYDMSG--AALALIL-----CVTKAREGSEDLDALEHMFRLQRFSTWKRDPFAEQ 60
Db 147 KDAVMSSRPGRMALIINRNFTCGMKERVGTDKDAENLYGLFWLGMATIRKDNLTGKA 206
2Y 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120
Db 207 MTRFEDLARRDHSAVD---CVVAILTHGISGLYSTDGLIPVEDLTGYFDGVNRPSL 263
2Y 121 RAKPKVVIQACRGEQDPG---ETVGG-----DEIVMVKDSPT- 158
Db 264 IGKPKVFVQACRGKDYGVSESTDGESYNKETANEMKQDFKVKVERALDADET 323
2Y 159 -----IFTYDHALHYSTVGTYAYRDQKGSFIQTLVDVF--TKRKHILELLE 208
Db 324 GGGYSREALTEADFLVAYATVPYVSWRNSEYGSWFIFAKFVDVTRDLASKEHFMDILTE 383
2Y 209 VTRMAEAEVQEGKARKTNPEIQ---STLRKLYLQ 242
Db 384 VNRKVA-----YDQSGRKNQIPAPVTMLTKLYR 415
RESULT 9
ID Q8MJU3 PRELIMINARY; PRT; 277 AA.
AC Q8MJU3
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Cysteine protease CPP32.
DC Oryctolagus cuniculus (Rabbit).
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
DX NCBI_TaxID=9986;
DX [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=98236830; PubMed=9575916;
RP Wang H., Keiser J.A.;
RP "Molecular characterization of rabbit CPP32 and its function in
RP vascular smooth muscle cell apoptosis.";
RP Am. J. Physiol. 274.H1132-H1140(1998).
RN [2]
RP SEQUENCE FROM N.A.
RP Wang H., Keiser J.A.;
RP Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF506008; AAM47195.1; -
GO; GO:0030693; F:caspace activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR00138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PF00656; Peptidase C14.
PRINTS; PR00376; ILIBCNZYME.
SMART; SM00115; CASc; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Protease.
SQ SEQUENCE 277 AA; 31653 MW; 7BA4B12E6D43629A CRC64;
Query Match 22.2%; Score 275.5; DB 6; Length 277;
Best Local Similarity 31.6%; Pred. No. 2.6e-15;
Matches 79; Conservative 39; Mismatches 105; Indels 27; Gaps 8;
QY 9 EKYDMSGALALILCVT-----KAREGSEDLDALEHMFRLQRFSTWKRDPFA 58
Db 34 DNSYKMDYPENGLCIIINKNFHKNTGSSRSGTDVNAANLGETFMNLKYEVRNKNDLTR 93
QY 59 EQQEELKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQ 118
Db 94 EEWELMNVNVEDHRSRFFC---VILSHDEGVIIYGTNGP-IELKLLTSFFRGDYCR 149
QY 119 ALRAKPKVVIQACRGEQDPG-ETVGGDEIVMVKDQFQIPTVTDALHYVSTVEGYIA 177
Db 150 SLATGPKLFIQACRGTELDGSIETDSGVYDMAC---QKIPVEADFLYAYSTAPGYTS 205
QY 178 YRDQKGSFIQTLVDVFTKRKHILE---LLTEVTRWA---EAEIVQEGKARKTNPE 230
Db 206 WRNSEGSGFIOGLC-AMUKYAHKLEFMHILTRNKRKVAETFEFSYSLDAFHAKKQIPC 264
QY 231 IQSTLRKRLY 240
Db 265 IVSMLTKELY 274
RESULT 10
ID Q8MJU1 PRELIMINARY; PRT; 277 AA.
AC Q8MJU1
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Caspase3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
OX [1]
RP SEQUENCE FROM N.A.
RP Yamazaki J., Sano J., Kano R., Hasegawa A.;
RP "Felis catus mRNA for caspase3, complete cds.";
RP Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB090246; BAC10589.1; -
GO; GO:0030693; F:caspace activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PF00656; Peptidase C14; 1.
PRINTS; PR00376; ILIBCNZYME.
SMART; SM00115; CASc; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
SEQUENCE 277 AA; 31465 MW; 8749679C30AB46F6 CRC64;
Query Match 22.2%; Score 275.5; DB 6; Length 277;
Best Local Similarity 33.3%; Pred. No. 2.6e-15;
Matches 84; Conservative 35; Mismatches 102; Indels 31; Gaps 10;
QY 9 EKYDMSGALALILCVTK-----ARGSEDLDALEHMFRLQRFSTWKRDPFA 58
Db 34 DNSYKMDYPENGLCIIINKNFHKNTGSSRSGTDVNAANLRETTNLKYEVRNKNDLTR 93
QY 59 EQQEELKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQ 118


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XX NCBI_TaxID=10090;
XN [1]
XP SEQUENCE FROM N.A.
XC STRAIN=FVE/N;
XA Strausberg R.;
AL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
JR EMBL; BC038825; AA38825.1; -.
JR MGD; MGI:107739; Casp3.
JR GO; GO:0030693; F:caspase activity; IEA.
JR GO; GO:0002333; P:peptidase activity; IEA.
JR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
JR InterPro; IPR002138; ICE_P10.
JR InterPro; IPR001309; ICE_P20.
JR InterPro; IPR002398; Peptidase_C14.
JR Pfam; PF00656; Peptidase_C14; 1.
JR PRINTS; PR00376; IL1BCENZME.
JR SMART; SM00115; CASc; 1.
JR PROSITE; PS01122; CASPASE_CYS; 1.
JR PROSITE; PS01121; CASPASE_HIS; 1.
JR PROSITE; PS0207; CASPASE_P10; 1.
JR PROSITE; PS0208; CASPASE_P20; 1.
JR PROSITE; PS0209; CASPASE_P10; 1.
JR PROSITE; PS0208; CASPASE_P20; 1.
JR PROTEASE.
TW NON TER
TT
IQ SEQUENCE 313 AA; 35174 MW; 96E98A1F04E769FC CRC64;

Query Match      22.1%; Score 273.5; DB 11; Length 313;
Best Local Similarity 34.8%; Pred. No. 4.4e-15;
Matches 77; Conservative 34; Mismatches 93; Indels 17; Gaps 7;

2Y 28 AREGSEEDLDALHMFRLQAFESTMKEDPTAEQFQBELEKFAQIDRSRDPVSCAFVILM 87
DB 99 SRSGTDVDAANLRRTFMGLKYQVKNKNDLTREDILELMDSVSKEDHSKSSFVC---VIL 155
2Y 88 AHGREGFLKGDGEMVKLENLFEALNNKNCQALRAKPKYIIQACRGQRDPG-ETVGGD 146
DB 156 SHGDEGVYGTNGP-VELKLTSTFRGDYCRSLTGPKPLIIQACRGTELDGCIETDSGT 214
2Y 147 EIVVMVKDSPTIPTYTDALHVVSTVGYIAYRHDKGSCFIQTLVDVFTFKRGHILE-- 204
DB 215 DEEMAC---QKIPVEADFLYATAGYYSWRNSKDGSMFISQSLCSML-KLYAHKLEFM 269
2Y 205 -LLTEVTRMA-----EAEVQEGKARTNTEIOTSLRKLY 240
DB 270 HILTRVNRKVATEFESFSLDSTFPAKQIPCTIVSMLTKEYL 310
[1]
RESULT 14
ID Q8MKI5 PRELIMINARY; PRT; 277 AA.
AC Q8MKI5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Caspase-3
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Sano J.;
RT "canine caspase-3 gene.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
JR EMBL; AB095580; BAB92962.1; -.
JR GO; GO:0030693; F:caspase activity; IEA.
JR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
JR InterPro; IPR002138; ICE_P10.
JR InterPro; IPR001309; ICE_P20.
JR InterPro; IPR002398; Peptidase_C14.
JR Pfam; PF00656; Peptidase_C14; 1.
JR PRINTS; PR00376; IL1BCENZME.
JR SMART; SM00115; CASc; 1.
JR PROSITE; PS01122; CASPASE_CYS; 1.
JR PROSITE; PS01121; CASPASE_HIS; 1.
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DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31334 MW; 7094C76D8686BDAB9 CRC64;

Query Match      22.0%; Score 272.5; DB 6; Length 277;
Best Local Similarity 33.5%; Pred. No. 4.6e-15;
Matches 84; Conservative 32; Mismatches 108; Indels 27; Gaps 9;

QY 9 EEKYDMSGAALALILCVTK-----AREGSEEDLDALHMFRLQAFESTMKEDPTA 58
DB 34 DNSYKMDYFEMGLCIINNNKNNFKSTGMAPRGSTDVDAANLRRTFMGLKYQVKNKNDLT 93
QY 59 EQFCELEKFAQIDRSRDPVSCAFVILMAHGRBFLKGDGEMVKLENLFEALNNKNCQ 118
DB 94 EEILELMNSVSKEDHSKSSFVC---VLLSHGDEGIIFGTNGP-VDLRKVTGFFRGDYCR 149
QY 119 ALRAKPKYIIQACRGQRDPG-ETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIA 177
DB 150 SLTGKPKPLIIQACRGTELDGCIETDSGIEDDMAC----QKIPVEADFLYATAGYYS 205
QY 178 YRHDKGSCFIQTLVDVFTFKRGHILE---LLTEVTRMA-EAEVQEGKA---RKTNPE 230
DB 206 WRNSKDGSMFISQSLC-AMKLYAHKLEFMHILTRVNRKVATEFESFSLDSTFPAKQIPC 264
QY 231 IQSTLRKLYL 241
DB 265 IVSMLTKEYL 275

RESULT 15
ID Q9IB63 PRELIMINARY; PRT; 399 AA.
AC Q9IB63;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038172; BAA94750.1; -.
DR HSSP; Q15806; 1ODU.
DR MESOPS; C14_010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016323; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
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R PROSITE; PS50207; CASPASE P10; 1.
R PROSITE; PS50208; CASPASE P20; 1.
R PROSITE; PS50017; DEATH DOMAIN; 1.
Q SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;
Query Match 22.0%; Score 272; DB 13; Length 399;
Best Local Similarity 27.9%; Pred. No. 8e-15;
Matches 80; Conservative 40; Mismatches 107; Indels 60; Gaps 8;
Y 2 SNERSLEEEK-YDMSGAAALALILCVT-----KAREGSEEDLDALAHMFRLRFES 50
b 125 SRKGTLDKDKDYPMSSDPDIFGCLIIINNNFHECTGLSTRGTSGDIDRDKLANRMSFHFV 184
Y 51 TMKRDPFABQFQEELEKFOQAIDSRDPVSCAFVVLMAHGRE-----GFLKGEDGEMV 103
b 185 TVKONLTGQAMHDLQALADQDHSLOD---CCLVILSHGCETRIQFFGGVYGTGIRI 241
Y 104 KLENLPEALNNKNCQALRAKPKYIIQACGEGQDPGETVGG----- 145
b 242 FVERIVSYFNGSKCPSLRGKPKFIIFQACGQDKQKGEVTSPTPLSPTSTLSQSDATP 301
Y 146 -----DEIVNVIKDSPQTIPTTDTALHVIYSTVEGYIAVHDQKSCFIQTLVDVFTK 197
b 302 VFSGEGDRDEV-----DAVSNIPSPDILVSYSTFPGYVSWEDKHTGWSYVEVLDSVLAE 356
Y 198 RKG--HILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKGLYLQ 242
b 357 HAAADQLQSLLVMV-----ADGVSSKGYKQIPGYFNFRLKRFYFK 397

earch completed: March 19, 2004, 11:24:12
ob time : 35.7092 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

run on: March 19, 2004, 11:09:05 ; Search time 9.64143 Seconds
(without alignments)
1306.961 Million cell updates/sec

title: US-09-989-903-5
effect score: 1239
sequence: 1 MSNPRSLSEKYMGAALA.....KARKTNPEIQTLRRLYLQ 242

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 141691 seqs, 52070155 residues

total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	1	ICEE_HUMAN
2	934.5	75.4	257	1	ICEE_MOUSE
3	305	24.6	424	1	ICEE_CHICK
4	295	23.8	435	1	ICEE_MOUSE
5	289	23.3	435	1	ICEE_HUMAN
6	279.5	22.6	277	1	ICEE_RAT
7	277.5	22.4	277	1	ICEE_CRIOLO
8	273.5	22.1	277	1	ICEE_MOUSE
9	272.5	22.0	277	1	ICEE_HUMAN
10	270	21.8	303	1	ICEE_MOUSE
11	260	21.0	303	1	ICEE_MOUSE
12	256	20.7	303	1	ICEE_MOUSE
13	248.5	20.1	503	1	ICED3_CAEEL
14	247.5	20.0	339	1	ICED3_MOUSE
15	246.5	19.9	479	1	ICED3_HUMAN
16	245	19.8	496	1	ICED3_CAEVU
17	240.5	19.4	276	1	ICED3_MOUSE
18	239.5	19.3	416	1	ICED3_HUMAN
19	237.5	19.2	299	1	ICED3_MOUSE
20	236.5	19.1	404	1	ICED3_MOUSE
21	233	18.8	480	1	ICED3_MOUSE
22	227	18.3	382	1	ICED3_MOUSE
23	226.5	18.3	382	1	ICED3_MOUSE
24	226	18.2	404	1	ICED3_MOUSE
25	225.5	18.2	323	1	ICED3_MOUSE
26	225	18.2	418	1	ICED3_MOUSE
27	222.5	18.0	385	1	ICED3_MOUSE
28	222	17.9	293	1	ICED3_MOUSE
29	221.5	17.9	521	1	ICED3_MOUSE
30	218.5	17.6	402	1	ICED3_MOUSE
31	218	17.6	373	1	ICED3_MOUSE
32	217.5	17.6	402	1	ICED3_MOUSE
33	213.5	17.2	312	1	ICED3_MOUSE

ALIGNMENTS

RESULT 1

ICED3_HUMAN STANDARD; PRT; 242 AA.

AC P31944; O95823; 405 1 IIBC_HORSE

DT 01-JUL-1993 (Rel. 26, Created) 410 1 IIBC_FELCA

DT 16-OCT-2001 (Rel. 40, Last sequence update) 404 1 IIBC_PIG

DT 15-MAR-2004 (Rel. 43, Last annotation update) 377 1 ICED_HUMAN

DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14). 377 1 ICED_BOVIN

GN CASP14. 419 1 ICED_MOUSE

OS Homo sapiens (Human). 419 1 ICED_MOUSE

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 484 1 CFLA_MOUSE

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 484 1 CFLA_MOUSE

OX NCBI_TaxID=9606; 484 1 CFLA_MOUSE

RN [1] 480 1 CFLA_HUMAN

RP SEQUENCE FROM N.A. 480 1 CFLA_HUMAN

RC TISSUE=Brain; 480 1 CFLA_HUMAN

RX MEDLINE=22168928; PubMed=12181750; 480 1 CFLA_HUMAN

RA Pistrutto G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L., 480 1 CFLA_HUMAN

RA Kari C., Lazebnik Y., Rodeck U., Alnemri E.S.; 480 1 CFLA_HUMAN

RT "Expression and transcriptional regulation of caspase-14 in simple 480 1 CFLA_HUMAN

RT and complex epithelia." 480 1 CFLA_HUMAN

RL Cell Death Differ. 9:995-1006(2002). 480 1 CFLA_HUMAN

RN [2] 480 1 CFLA_HUMAN

RP SEQUENCE OF 68-74; 137-147 AND 154-162. 480 1 CFLA_HUMAN

RC TISSUE=keratinocytes; 480 1 CFLA_HUMAN

RX MEDLINE=93162043; PubMed=1286667; 480 1 CFLA_HUMAN

RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., 480 1 CFLA_HUMAN

RA Vandekerckhove J.; 480 1 CFLA_HUMAN

RT "Microsequences of 145 proteins recorded in the two-dimensional gel 480 1 CFLA_HUMAN

protein database of normal human epidermal keratinocytes." 480 1 CFLA_HUMAN

RL Electrophoresis 13:960-969(1992). 480 1 CFLA_HUMAN

CC -!- FUNCTION: May be involved in the death receptor and granzyme B 480 1 CFLA_HUMAN

apoptotic pathways. May function as a downstream signal transducer 480 1 CFLA_HUMAN

of cell death. 480 1 CFLA_HUMAN

-!- SUBUNIT: May dimerize with large prodomain caspases. 480 1 CFLA_HUMAN

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). 480 1 CFLA_HUMAN

-!- SIMILARITY: Belongs to peptidase family C14. 480 1 CFLA_HUMAN

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or send an email to license@isb-sib.ch). 480 1 CFLA_HUMAN

EMBL; AF097874; AAD16173.1; 480 1 CFLA_HUMAN

PIR; JC7517; JC7517. 480 1 CFLA_HUMAN

HSSP; P29466; IICE. 480 1 CFLA_HUMAN

DR Aarhus/Ghent-2DPAGE; 6109; IEF. 480 1 CFLA_HUMAN

DR MEROPS; C14.018; 480 1 CFLA_HUMAN

DR Genew; HGNC:1502; CASP14. 480 1 CFLA_HUMAN

DR MIN; 605848; 480 1 CFLA_HUMAN

DR GO; GO:0004199; F:caspase activity; TAS. 480 1 CFLA_HUMAN

DR GO; GO:0008544; P:epidermal differentiation; TAS. 480 1 CFLA_HUMAN

DR InterPro; IPR002138; ICE_p10. 480 1 CFLA_HUMAN


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3 InterPro; IPR001309; ICE_P20.
4 InterPro; IPR002398; Peptidase C14.
5 Pfam; PF00656; Peptidase C14; 1.
6 PRINTS; PRO0376; ILBCEZYME.
7 SMART; SM00115; CASP. 1.
8 PROSITE; PS01121; CASPASE HIS; FALSE NEG.
9 PROSITE; PS01122; CASPASE_CYS; FALSE NEG.
10 PROSITE; PS02027; CASPASE_P10; 1.
11 PROSITE; PS02028; CASPASE_P20; 1.
12 Hydrolase; Thiol protease; Apoptosis; Zymogen.
13 PROPEP 1 ?
14 CHAIN ? 146
15 SUBUNIT ? 146
16 TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain
17 ACT SITE 89
18 BY SIMILARITY.
19 ACT SITE 132
20 BY SIMILARITY.
21 SEQUENCE 242 AA; 27679 MW; E539F7E8DD808A2 CRC64;

Query Match 99.6%; Score 1234; DB 1; Length 242;
Best Local Similarity 99.6%; Pred. No. 5.8e-92;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 1 MGNPSLEEKYDMSGAALALILCVTKAREGSEEDLDALHMFQRLFEFTMKRDPTEAQ 60
2 1 MGNPSLEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLFEFTMKRDPTEAQ 60
3 61 FQEELEKFOAIDSDREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
4 61 FQEELEKFOAIDSDREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
5 121 RAKPKVYIIQACRGQRDPGEVGVGDEIWMVKSPQIPIYTDALHVSIVTEGYIAYRH 180
6 121 RAKPKVYIIQACRGQRDPGEVGVGDEIWMVKSPQIPIYTDALHVSIVTEGYIAYRH 180
7 181 DQKGSFCIQLVDVFTKRGHILELLTEVTRMAAEIVQEGKARKNPFIQSTLRKELY 240
8 181 DQKGSFCIQLVDVFTKRGHILELLTEVTRMAAEIVQEGKARKNPFIQSTLRKELY 240
9 241 LQ 242
10 241 LQ 242

ESULT 2
CEE MOUSE STANDARD; PRT; 257 AA.
C Q89034;
T 16-OCT-2001 (Rel. 40, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 15-MAR-2004 (Rel. 43, Last annotation update)
E Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (Mini-ICE) (MICE).
N CASP14.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
P [1]
P SEQUENCE FROM N.A., AND CHARACTERIZATION.
C C C57BL/6J;
X MEDLINE=99040667; PubMed=9823333;
A Ahmad M., Srinivasula S.M., Hegde R., Mukattash R.,
A Fernandes-Alnemri T., Alnemri E.S.,
A Vandenabeele P.,
T "Identification and characterization of murine caspase-14, a new
T member of the caspase family."
T Cancer Res. 58:5201-5205(1998).
L [2]
N SEQUENCE FROM N.A.
P STRAIN=C57BL/6; TISSUE=Embryo;
X MEDLINE=99222069; PubMed=10203698;
A Van de Craen M., Van Ico G., Pyke S., Van Crieckinge W.,
A Vandenabeele P.,
T "Identification of a new caspase homologue: caspase-14."
T Cell Death Differ. 5:838-846(1998).
L
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RN RP CHARACTERIZATION, AND MUTAGENESIS OF CVS-136.
RX MEDLINE=99009076; PubMed=9792675;
RA Hu S., Snipas S.J., Vincenz C., Salvesen G., Dixit V.M.;
RT "Caspase-14 is a novel developmentally regulated protease."
RL J. Biol. Chem. 273:29648-29653(1998).
CC -!- FUNCTION: Seems to be involved in the death receptor and granzyme
CC B apoptotic pathways. May function as a downstream signal
CC transducer of cell death. May play a role in ontogenesis and skin
CC physiology.
CC -!- SUBUNIT: May dimerize with large prodomain caspases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
CC -!- TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain
CC and kidney.
CC -!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF092997; AAC63364.1; -.
CC EMBL; AJ007750; CAA07678.1; -.
CC HSSP; P29466; 1ICE.
CC MEROPS; C14.018; -.
CC MGD; MGI:1335092; Casp14.
CC GO; GO:0006917; P:induction of apoptosis; IDA.
CC InterPro; IPR002138; ICE_P10.
CC InterPro; IPR001309; ICE_P20.
CC InterPro; IPR002398; Peptidase_C14.
CC Pfam; PF00656; Peptidase_C14; 1.
CC PRINTS; PRO0376; ILBCEZYME.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS01121; CASPASE HIS; FALSE NEG.
CC PROSITE; PS01122; CASPASE_CYS; FALSE NEG.
CC PROSITE; PS02027; CASPASE_P10; 1.
CC PROSITE; PS02028; CASPASE_P20; 1.
CC Hydrolase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 7
FT CHAIN 8 ?
FT CASPASE-14 SUBUNIT P18 (POTENTIAL).
FT CHAIN 2 257
FT CASPASE-14 SUBUNIT P11 (POTENTIAL).
FT ACT SITE 93
FT BY SIMILARITY.
FT ACT SITE 136
FT BY SIMILARITY.
FT ACT SITE 136
FT C->A: DECREASE IN DEATH-INDUCING
FT MUTAGEN 136
FT ACTIVITY.
SQ SEQUENCE 257 AA; 29458 MW; A228D8DFBA0EB84 CRC64;

Query Match 75.4%; Score 934.5; DB 1; Length 257;
Best Local Similarity 70.9%; Pred. No. 6.5e-68;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MGNPSLEEKYDMSGAALALILCVTKAREGSEEDLDALHMFQRLFEFTMKRDPTEAQ 60
DB 5 MSDPQLOEYDMSGARLALILCVTKAREGSEEDMEALERNFYLKFEFTMKRDPTEAQ 64
QY 61 FQEELEKFOAIDSDREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 65 FLEELDEFQQTIDNWESEPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCAL 124
QY 121 RAKPKVYIIQACRGQRDPGEVGVGDEIWMVKSPQIPIYTDALHVSIVTEGYIAYRH 168
DB 125 RAKPKVYIIQACRGQRDPGEVGVGDEIWMVKSPQIPIYTDALHVSIVTEGYIAYRH 183
QY 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRGHILELLTEVTRMAAEIVQEGKARKNP 228
DB 184 YSTVEGYLSYRHDGSGFIQTLVDVFTKRGHILELLTEVTRMAAEIVQEGKARKNP 243
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229 PEOSTLRKLYLQ 242
 244 PEVOSTLRKLYLQ 257

RESULT 3
 ICE2 CHICK STANDARD; PRT; 424 AA.
 ID Q88943;
 01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).
 CASP2 OR ICH1.
 Gallus gallus (Chicken).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 NCBI_TaxID=9031;
 [1]
 SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).
 STRAIN=White leghorn; TISSUE=Ovarian granulosa;
 MEDLINE=97368127; PubMed=9224894;
 Johnson A.B., Bridgham J.T., Bergeron L., Yuan J.;
 "Characterization of the avian Ich-1 cDNA and expression of Ich-1L mRNA in the hen ovary";
 Gene 192:227-233(1997).
 !- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Might function by either activating some proteins required for cell death or inactivating proteins necessary for cell survival (By similarity).
 !- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=ICH-1L;
 IsoId=Q88943-1; Sequence=Displayed;
 Note=Only form found in the ovary;
 Name=ICH-1S;
 IsoId=Q88943-2; Sequence=VSP 000803, VSP 000804;
 !- PTM: Heterodimer of a small and a large subunit (By similarity).
 !- SIMILARITY: Belongs to peptidase family C14.
 !- SIMILARITY: Contains 1 CARD domain.

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EMBL: U64963; AAC29881.1; ALT_INIT.
 HSRF; P42574; ICP3.
 MEROPS: C14.006; -
 InterPro: IPR001315; CARD.
 InterPro: IPR002138; ICE p10.
 InterPro: IPR001309; ICE p20.
 InterPro: IPR002398; Peptidase_C14.
 Pfam: PF00619; CARD; 1.
 Pfam: PF00656; Peptidase_C14; 1.
 PRINTS: PR00376; ILIACENZYME.
 SMART: SM00114; CARD; 1.
 SMART: SM00115; CARD; 1.
 PROSITE: PS02029; CARD; 1.
 PROSITE: PS01122; CASPASE_CYS; 1.
 PROSITE: PS01121; CASPASE_HIS; 1.
 PROSITE: PS02027; CASPASE_P10; 1.
 PROSITE: PS02028; CASPASE_P20; 1.
 PROSITE: PS02029; CASPASE_P20; 1.
 Hydrolase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
 PROPEP 1 140
 CHAIN 141 308 BY SIMILARITY.
 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
 CHAIN 309 424

FT CHAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
 FT DOMAIN 7 96 CARD.
 FT ACT_SITE 248 248 BY SIMILARITY.
 FT ACT_SITE 291 291 Missing (in isoform ICH-1S).
 FT VARSPLIC 1 7 /FTId=VSP 000803.
 FT VARSPLIC 294 424 DETDGVQDQDQKERSDSDSPGCEESDANKEENIKLKLPTPSD
 MICGVACLKGTAAKNTKRGSWIIEALITVFAEDSRDTHVA
 DMLVKNRQIKQEGYAPGTEFHRCKEMSEYCSLCLRDLYL
 FPGYVFGK -> GVSQIHLPLPCCHCICCSMRQTEWI
 REMXNGQIQPOAVRRVMQTRKKISSVCVCLHAPI (in
 isoform ICH-1S).
 /FTId=VSP 000804.
 FT VARSPLIC 294 424 /FTId=VSP 000804.
 SQ SEQUENCE 424 AA; 47959 MW; 792810508B8B2F60 CRC64;
 Query Match 24.6%; Score 305; DB 1; Length 424;
 Best Local Similarity 31.5%; Pred. No. 3.7e-17;
 Matches 86; Conservative 51; Mismatches 82; Indels 54; Gaps 10;
 QY 1 MSNPRSEEEKYDMSGAALALILC-----VTKAREGSEEDLDALHMPRQLFFESTM 52
 DB 166 ISBPR-----GLALLILSNTHFSKXDLVRSKGGVDVDCASLELLFKHLYGYQTV 213
 QY 53 KRDPTRFQFOELEKFOQAIIDSRDPVSCAFVYVMAHGREGLKGDGEMVXLENLFPAL 112
 DB 214 FHDQSAEMESALERSFKLPD-HQVDVSC-IVALLSHGVGGVGTGDKLQLQEAFLF 271
 QY 113 NNKVCQALRAKPKVYIIQACRGEQDPG-ETVGGDEIVMVKDSP-----Q 157
 DB 272 DNANCPNLQNKPKMFFIQACRGDETGRGVQDQDQKE-----RSDSPGCEESDANKEENIKL 327
 QY 158 TIPTYTDALHVGTVGTYAYRHQDQSGCFIOTLVNDVFTK--RKHILELLTEVTRRVAE 215
 DB 328 RLPTFRSDMICGYACLKGTAAKNTKRGSWIIEALITVFAEDSRDTHVADMLVKNRQIKQ 387
 QY 216 AELVQEGKARKTN-----PEQSTLRKLYL 241
 DB 388 ----REGYAPGTEFHRCKEMSEYCSLCLRDLYL 416

RESULT 4
 ICE2 MOUSE STANDARD; PRT; 435 AA.
 ID ICE2_MOUSE
 AC P29594; O08737;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2 protein).
 GN CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALEB/C;
 RX MEDLINE=95047319; PubMed=7958843;
 RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
 "Induction of apoptosis by the mouse Nedd2 gene, which encodes a protein similar to the product of the Caenorhabditis elegans cell death gene ced-3 and the mammalian IL-1 beta-converting enzyme";
 Genes Dev. 8:1613-1626(1994).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C3H/AN;
 RX MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I., van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R., Fiers W.;
 "Characterization of seven murine caspase family members";
 FEBS Lett. 403:61-69(1997).
 RN [3]

P PRELIMINARY PARTIAL SEQUENCE FROM N.A.
MEDLINE=92228780; PubMed=1378265;
Kumar S., Tomooka Y., Noda M.;
"Identification of a set of genes with developmentally down-regulated
expression in the mouse brain."
Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
-!- FUNCTION: Involved in the activation cascade of caspases
responsible for apoptosis execution. Might function by either
activating some proteins required for cell death or inactivating
proteins necessary for cell survival. May be important in
multistep carcinogenesis.
-!- SUBUNIT: Heterodimer of a small and a large subunit (By
similarity).
-!- TISSUE SPECIFICITY: High level expression seen in the embryonic
CNS, liver, lung, kidney, small intestine, and hair follicles of
vibrissae. Moderate expression seen in the skin, oral mucosa,
skeletal muscle, submandibular gland and thymus. In the adult, it
is highly expressed in spleen, lung and kidney. Moderately in the
brain, heart, testis, liver. Low levels in the thymus, skeletal
muscle, ovary and gut.
-!- DEVELOPMENTAL STAGE: During embryonic development is highly
expressed in several types of mouse tissue undergoing high rates
of programmed cell death such as central nervous system and
kidney.
-!- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
THAT OF OTHER CASPASES (BY SIMILARITY).
-!- SIMILARITY: Belongs to peptidase family C14.
-!- SIMILARITY: Contains 1 CARD domain.

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or send an email to license@sib-sib.ch).

EMBL; D28492; BAA25876.1; ALT INIT.
EMBL; Y13085; CAA73527.1; ALT_INIT.
HSP; P42574; ICP3.
MEROPS; C14.006; --.
MGD; MGI:97295; Casp2.
InterPro; IPR001315; CARD.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; ILIBENZYME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASC; 1.
PROSITE; PS0209; CARD; 1.
PROSITE; PS0122; CASPASE_CYS; 1.
PROSITE; PS0121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Apoptosis; Zymogen.
PROPEP 1 152 BY SIMILARITY.
T CHAIN 153 316 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
T CHAIN 317 435 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
T CHAIN 331 435 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
T CHAIN 331 435 CARD.
T DOMAIN 15 103 CARD.
T ACT_SITE 260 260 BY SIMILARITY.
T ACT_SITE 303 303 BY SIMILARITY.
T MUTAGEN 303 303 C->G: LOSS OF FUNCTION.
T CONFLICT 71 71 MISSING (IN REF. 1).
Q SEQUENCE 435 AA; 48896 MW; 8984E6AA767A676 CRC64;

Query Match 23.8%; Score 295; DB 1; Length 435;
Best Local Similarity 31.5%; Pred. No. 2.4e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY 29 REGSEEDLAEHMFRLQRPSTWKRDPPTAEQFQEBLEKFKQQAIDSRDPVSCAFVILMA 88
Db 202 RSGGDVHTTTLVTLFKLLGYNVHVLHDQTAQEQKLNQFAQ-LPAHRVTDSCV-VALLS 259
QY 89 HGRGFLKGDGEMVWKLNFALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
Db 260 HGVGGYGVGDGKLLQJQEVFRLFDNANCSLQNKPKPFFIQACRDETDGVDQDQGN 319
QY 141 -----ETVGGDEIVWVKDSPTIPTYTDALHYVSTVEGYIAYRHQKSCFQTLLV 192
Db 320 HTQSPGCCESDAGKEELMKVR-----LPTSDMICGVACLKGNAMRNTKRGSWYTEALT 374
QY 193 DVFTKR--KGHILELLETVTRMAEALVQEGKARKTN-----PEIQSTLEKRLYL 241
Db 375 QVFSERACDMHVDMLVKVNALIKE----REGYAPGTFFHRCCKEMSEYCSLCCQQLYL 428
RESULT 5
ICE2_HUMAN
ID ICE2_HUMAN STANDARD; PRT: 435 AA.
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
1L/1S)
GN CASP2 OR ICH1
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Fetal brain;
RX MEDLINE=94373811; PubMed=8087842;
RA Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;
"Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
regulators of programmed cell death."
RL Cell 78:739-750(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ALA-161 AND
RP GLY-424.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
Miyamoto K.E., Nguyen C.P., Nguyen D.A., Foel C.L., Robertson F.D.,
Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Doeberer A., Martinka S., Maupin R.;
Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CLEAVAGE SITES.
RX MEDLINE=96206041; PubMed=8654923;
RA Xue D., Shaham S., Horvitz H.R.;
"The Casnorchaditis elegans cell-death protein CED-3 is a cysteine
protease with substrate specificities similar to those of the human
CPP32 protease."
RT Genes Dev. 10:1073-1083(1996).
RL CC
CC -!- FUNCTION: Involved in the activation cascade of caspases
responsible for apoptosis execution. Might function by either
activating some proteins required for cell death or inactivating
proteins necessary for cell survival.
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By
similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ in the N- and C-termini;
CC Name=ICH-1L;
CC IsoID=P42575-1; Sequence=Displayed;
CC Note=Acts as a positive regulator of apoptosis;
CC Name=ICH-1S;
CC IsoID=P42575-2; Sequence=VSP 000801, VSP 000802;
CC Note=Acts as a negative regulator of apoptosis;

-!- TISSUE SPECIFICITY: Expressed in larger amounts in the embryonic lung, liver and kidney than in the heart and brain. In the adults higher level expression is seen in the placenta, lung, kidney, pancreas than in the heart, brain, liver and skeletal muscle.
 -!- PFM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT THAT OF OTHER CASPASES.
 -!- SIMILARITY: Belongs to peptidase family C14.
 -!- SIMILARITY: Contains 1 CARD domain.

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 EMBL; U13021; AA58959.1; --
 EMBL; U13022; AA58960.1; --
 EMBL; AY219042; ARO25653.1; --
 EMBL; AC073342; AAP22346.1; --
 PIR; A54821; A54821.
 HSP; P29466; 1ICE.
 MEROPS; C14.006; --
 Genew; HGNC:1503; CASP2.
 MIM; 600639; --
 GO; GO:0004202; F:caspase-2 activity; TAS.
 GO; GO:0018899; F:enzyme binding; TAS.
 GO; GO:0008632; P:apoptotic program; TAS.
 GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 InterPro; IPR001315; CARD.
 InterPro; IPR002138; ICE_p10.
 InterPro; IPR001309; ICE_p20.
 InterPro; IPR002398; Peptidase_C14.
 Pfam; PF00656; CARD; 1.
 Pfam; PF00656; Peptidase_C14; 1.
 PRINTS; PR00376; IL1BENZYM.
 SMART; SM01114; CARD; 1.
 SMART; SM01115; CASG; 1.
 PROSITE; PS02029; CARD; 1.
 PROSITE; PS01121; CASPASE_CYS; 1.
 PROSITE; PS01122; CASPASE_HIS; 1.
 PROSITE; PS02027; CASPASE_P10; 1.
 PROSITE; PS02028; CASPASE_P20; 1.
 Hydrolase; Thiol protease; Apoptosis; Zymogen; Polymorphism;
 Alternative splicing
 PROPEP 1 152 CASPASE-2 SUBUNIT P18.
 CHAIN 153 308 CASPASE-2 SUBUNIT P13.
 PROPEP 309 316 CASPASE-2 SUBUNIT P12.
 CHAIN 317 435 CARD.
 CHAIN 331 435 BY SIMILARITY.
 DOMAIN 15 103 BY SIMILARITY.
 ACT_SITE 260 260 Missing (in isoform ICH-18).
 ACT_SITE 303 303 /FTid=VSP_000801.
 VARSPLIC 1 14 /FTid=VSP_000801.
 VARSPLIC 306 435 DETDRGVDDQDGNHAGSPGCEESDAGKELPKMLPTPSD
 MICYACLGKTAAMRNTKRGSWYIEALAOVFSERACDMHVA
 DMLVKVNLKIDREGVAPGTEPHRCKEMSEYCSLCHLYL
 FPGHPPT -> GEAISGLHLLFTATASLAL (in isoform ICH-18).
 /FTid=VSP_000802.
 V -> L. /FTid=VAR_016334.
 P -> A. /FTid=VAR_016335.
 R -> G. /FTid=VAR_016336.
 C -> S. LOSS OF FUNCTION.
 A -> T. LOSS OF FUNCTION.
 SEQUENCE 435 AA; 48855 MW; 1652EC73F6286FE7 CRC64;
 Query Match 23.3%; Score 289; DB 1; Length 435;

Best Local Similarity 31.1%; Pred. No. 7.3e-16;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
 QY 29 REGSEEDLDALHMPFQRLPFESTMKRDPDTAEQFQELKFOQADSDREDPVSCAFVVLMA 88
 DB 202 RSGGDVHSTLTLFKLLGYDVHVLCDQTAQEMQKLFQFAQ-LPAHRVTDSC-IVALLS 259
 QY 89 HGREGLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDFG----- 140
 DB 260 HGVEGAIYGVQDKLLQLQVQFQFQACRGGDETDGRGVQDQDGN 319
 QY 141 -----FTVGDEIVMVKSPQPTIYTDALHVTYGVGYAYRHDKGSCFIQTLV 192
 DB 320 HAGSPCEESDAGKE-----KLPKVRLPTRSDMICYACLGKTAAMRNTKRGSWYIEALA 374
 QY 193 DVFTK3--KGHILELITVTRMAEALVQEGKAKTN-----PEIQSLRKELYL 241
 DB 375 QVFSERACDMHVMVKNALIKD-----REGVAGTEPHRCKEMSEYCSLCHRLYL 428

 RESULT 6
 ID ICE3 RAT STANDARD; PRT; 277 AA.
 AC P55213; P70543; P97699; Q62993;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptain precursor (BC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1) (SCA-1) (LICE) (IRP).
 DE CASP3 OR CPP32.
 GN Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.-S.-C. McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G., Fletcher F.A.,
 RA "Molecular characterization of mouse and rat CPP32 beta gene encoding a cysteine protease resembling interleukin-1 beta converting enzyme RT and CED-3".
 RL Oncogene 13:749-755(1996).
 RN [2]
 RP SEQUENCE OF 30-241 FROM N.A.
 RC TISSUE=Ovary; PubMed=7588240;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
 RA Hirshfield A.N., Tilly J.L.;
 RA "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cells of the ovarian follicle".
 RL Endocrinology 136:5042-5053 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184204; PubMed=9030616;
 RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
 RA Rostek P. Jr., Poirier G.G., Paul S.M.;
 RA "Cloning and expression of a rat brain interleukin-1beta-converting enzyme (ICE)-related protease (IRP) and its possible role in apoptosis of cultured cerebellar granule neurons".
 RL J. Neurosci. 17:1561-1569(1997).
 RN [4]
 RP SEQUENCE OF 1-264 FROM N.A.
 RA Yakovlev A.G.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. At the onset of apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase (PAR) at a 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory

element binding proteins (SREBPs) between the basic helix-loop-helix leucine zipper domain and the membrane attachment domain. Cleaves and activates caspase-6, -7 and -9 (By similarity).

-!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE BUT NOT IN KIDNEY OR TESTIS.

-!- DEVELOPMENTAL STAGE: Highly expressed in neuron-enriched regions of the developing brain, but down-regulated to low levels in the adult brain.

-!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND VICE VERSA (BY SIMILARITY).

-!- SIMILARITY: Belongs to peptidase family C14.

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EMBL; U49930; AAC52765.1; -

EMBL; U34685; AAC52261.1; -

EMBL; U84410; AAB41792.1; -

EMBL; U58656; AAB02722.1; -

PIR; I67437; I67437.

HSSP; P42574; 1PAU.

MEROPS; C14.003; -

InterPro; IPR002138; ICE_p10.

InterPro; IPR002398; Peptidase_C14.

InterPro; P800656; Peptidase_C14; 1.

PRINTS; PR00376; ILIBENZYM.

SMART; SM00115; CASC; 1.

PROSITE; PS01122; CASPAGE_CVS; 1.

PROSITE; PS01221; CASPAGE_HIS; 1.

PROSITE; PS02077; CASPAGE_P10; 1.

PROSITE; PS02088; CASPAGE_P20; 1.

Hydrolase; Thiol protease; Zymogen; Apoptosis.

PROPER; 1 9 BY SIMILARITY.

PROPER; 10 28 BY SIMILARITY.

CHAIN; 176 277 APOPTIN P17 SUBUNIT.

CHAIN; 121 121 APOPTIN P12 SUBUNIT.

ACT_SITE; 163 163 KMSD -> QVD (IN REF. 4).

CONFLICT; 170 170 C -> S (IN REF. 2).

CONFLICT; 178 178 T -> A (IN REF. 2).

CONFLICT; 182 182 I -> V (IN REF. 2).

CONFLICT; 187 187 M -> K (IN REF. 2).

CONFLICT; 190 190 E -> G (IN REF. 3).

CONFLICT; 199 199 D -> S (IN REF. 2).

CONFLICT; 211 211 T -> G (IN REF. 2).

CONFLICT; 236 236 L -> I (IN REF. 4).

CONFLICT; 245 245 T -> M (IN REF. 3).

SEQUENCE; 277 AA; ADABF418E2507402 CRC64;

Query Match 22.8%; Score 279.5; DB 1; Length 277;

Best Local Similarity 32.8%; Pred. No. 2.4e-15;

Matches 82; Conservative 35; Mismatches 106; Indels 27; Gaps 8;

Y 9 EEKYMDSGAALAILCVT-----KARGESEEDLDALEHMFQRLRFSTMKRDTFA 58

b 34 DSSVYMDYFPEWGLCIINNNKFNHFKSGMSARNGTDVDAANLRETFWALGVYRNKNDLTR 93

Y 59 EQFOELEKFCQQAIDSRDDPVSCAFVVLVAHGREGLKGEDEMKLENLFEALNNKQC 118

Db 94 EEIMELMDSVSKEDHSKRSSFVC---VILSHGDEGVIFGTNGP-VDLKLTSPFRGDYCR 149

Qy 119 ALRAKPKVYIIQACRGEQDPG-ETVGDIEIVMWKDSQTIPTTDLALHYSTVEGYIA 177

Db 150 SLATGPKLFIIQACRGTETDCGTDGTTDDMAC-----QKIPVADFLYAYSTAPGYIS 205

Qy 178 YRDQKSGCFIQLVDVFTKRKHILE---LLETVTRMA-----EAEIVQEGKARKTNPE 230

Db 206 WNRSDGSWEIQLC-AMUKLYAKLEFHEILTRVNRKVATEFESFSLDATEHAKQIPC 264

Qy 231 IQSTLRKRLY 240

Db 265 IVSMLTKELY 274

RESULT 7

ICE3_CRILLO STANDARD; PRT; 277 AA.

ID ICE3_CRILLO

AC Q60431;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 15-MAR-2004 (Rel. 43, Last annotation update)

DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1) (SCA-1).

DE (CASP3 OR CPP32).

GN Crictetus longicaudatus (Long-tailed hamster) (Chinese hamster).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; OC Crictetus.

OC NCBI_taxid=10030;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=96183185; PubMed=8605870;

RA Wang X., Zelenski N.G., Yang J., Sakai J., Brown M.S., Colstain J.L.;

RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during apoptosis."

RL EMBO J. 15:1012-1020(1996).

CC -!- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. At the onset of apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory element binding proteins (SREBPs) between the basic helix-loop-helix leucine zipper domain and the membrane attachment domain. Cleaves and activates caspase-6, -7 and -9 (By similarity). subunit

CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND VICE VERSA (BY SIMILARITY).

CC -!- SIMILARITY: Belongs to peptidase family C14.

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EMBL; U27463; AAB01511.1; -

HSSP; P42574; 1PAU.

MEROPS; C14.003; -

InterPro; IPR002138; ICE_p10.

InterPro; IPR001309; ICE_p20.

InterPro; IPR002398; Peptidase_C14.

Pfam; PF00656; Peptidase_C14; 1.

R PRINTS; PRO0376; IL1BCENZME.
R SMART; SM01115; CASC; 1.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS0207; CASPASE_P10; 1.
R PROSITE; PS0208; CASPASE_P20; 1.
W Hydrolase; Thiol protease; Zymogen; Apoptosis.
T PROPEP 1 9 BY SIMILARITY.
T PROPEP 10 28 APOPAIN P17 SUBUNIT.
T CHAIN 29 175 APOPAIN P12 SUBUNIT.
T CHAIN 176 277 APOPAIN P12 SUBUNIT.
T ACT_SITE 121 121 BY SIMILARITY.
T ACT_SITE 163 163 BY SIMILARITY.
Q SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;

Query Match 22.4%; Score 277.5; DB 1; Length 277;
Best Local Similarity 35.9%; Pred. No. 3.4e-15;
Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;

Y 29 REGSEEDLDALEHMFOLRFESTWMDPTAQFQBELEKFOAIDSRDFVSCAFVVLMA 88
b 64 RSGTDDVDAKLRETFWALKYEVKNKDLTREIEIVLMKNASKEDSKRSFVC---VILS 120
y 89 HGRGFLKGDGEWKLLENFEALNNKCOALRAKPKVIIQACGEQDPOG-ETVGGDE 147
b 121 HGDEVIPTGIDGP-IDLKULTSVFRGDYKSLICKPKLFIQACRGTELDGCIETDSGTE 179
y 148 IVMVIKDSQPTIPTYTDALHYSTVEGYTAHRDQKSGCFITGLVDVFTFKRGHILE--- 204
b 180 DDMTC---QKIPVEADFLVAYSTAPGYYSWRNPKDGSWFIQSLCSML-KLYAHKLEFMH 234
y 205 LITVTRMA-----EALVQEGKARTNPEIQSTLEKLY 240
b 235 ILTVNRKRVATEFESFSLDSTFFAKQIQCIVSNLTKEYL 274

RESULT 8
ICE3 MOUSE STANDARD; PRT; 277 AA.
ID ICE3 MOUSE STANDARD; PRT; 277 AA.
Y 070677; O08668; Q9QW14;
Y 01-NOV-1997 (Rel. 35, Created)
Y 15-MAR-2004 (Rel. 43, Last annotation update)
Y Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-3) (LICE)
EN CASP3 OR CPP32.
CS Mus musculus (Mouse).
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI TaxID=10090;
X [1]
X SEQUENCE FROM N.A.
X MEDLINE=96358624; PubMed=8761296;
X Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
X Fletcher F.A.;
X "Molecular characterization of mouse and rat CPP32 beta gene encoding
X a cysteine protease resembling interleukin-1 beta converting enzyme
X and CED-3";
X Oncogene 13:749-755 (1996).
X [2]
X SEQUENCE FROM N.A.
X MEDLINE=97224429; PubMed=9070890;
X Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
X "Specific expression of CPP32 in sensory neurons of mouse embryos and
X activation of CPP32 in the apoptosis induced by a withdrawal of
X NGF";
X Biochem. Biophys. Res. Commun. 231:770-774 (1997).
X [3]
X SEQUENCE FROM N.A.
X STRAIN=C3H/An;
X MEDLINE=97190206; PubMed=9038361;
X van de Craen M., Vandenberghe P., Declercq W., van den Brande I.,

van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
Fiers W.;
"Characterization of seven murine caspase family members.";
FEBS Lett. 403:61-69 (1997).
[4]
R SEQUENCE FROM N.A.
R TISSUE=Brain;
R Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
R Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[5]
R SEQUENCE FROM N.A.
R STRAIN=FVB/N; TISSUE=Mammary gland;
R MEDLINE=22388257; PubMed=1247932;
R Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,
R Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
R Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
R Atschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
R Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
R Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
R Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
R Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
R Vallalón D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R Mahting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
R Butterfield Y.S., Krzywinski M.I., Skalska U., Smalhus D.E.,
R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
R "Generation and initial analysis of more than 15,000 full-length
R human and mouse cDNA sequences.";
R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[6]
R SEQUENCE OF 58-277 FROM N.A.
R Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
R Fortin J.-P., Sekaly R.-P.;
R "Multiple pathways of apoptosis converging on the CPP32 protease.";
R Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
R -1- FUNCTION: Involved in the activation cascade of caspases
R responsible for apoptosis execution. At the onset of apoptosis it
R proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
R 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
R element binding proteins (SREBPs) between the basic helix-loop-
R helix leucine zipper domain and the membrane attachment domain.
R Cleaves and activates caspase-6, -7 and -9 (By similarity).
R Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
R cytokine which is involved in a variety of inflammatory processes.
R -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
R (By similarity).
R -1- SUBCELLULAR LOCATION: Cytoplasmic.
R -1- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
R kidney and heart. Lower expression in brain, skeletal muscle and
R testis.
R -1- PTM: CLEAVAGE BY GRANTZYME B. CASPASE-6, -8 AND -10 GENERATES THE
R TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
R LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
R PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
R CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
R VICE VERSA (BY SIMILARITY).
R -1- SIMILARITY: Belongs to peptidase family C14.

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R between the Swiss Institute of Bioinformatics and the EMBL outstation -
R the European Bioinformatics Institute. There are no restrictions on its
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R entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
R or send an email to license@sib-sib.ch).

R EMBL; U54803; AAC52768.1; -;
R EMBL; U54802; AAC52768.1; JOINED.
R EMBL; U49929; AAC52764.1; -;

Nat. Struct. Biol. 3:619-625(1996).
[8]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
MEDLINE=97197830; PubMed=9045680;
Mittel P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
Priestle J.P., Tomaselli K.J., Gruetter M.G.;
"Structure of recombinant human CPP32 in complex with the
tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone";
J. Biol. Chem. 272:6539-6547(1997).
[9]
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=20283632; PubMed=10821855;
Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
Levy M.A., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
"Potent and selective nonpeptide inhibitors of caspases 3 and 7
inhibit apoptosis and maintain cell functionality";
J. Biol. Chem. 275:16007-16014(2000).
[10]
PROCESSING.
MEDLINE=96353838; PubMed=8755496;
Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
Litwack G., Alnemri E.S.;
"In vitro activation of CPP32 and Mch3 by Mch4, a novel human
apoptotic cysteine protease containing two FADD-like domains";
Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
[11]
CLEAVAGE OF HUNTINGTIN
MEDLINE=96331283; PubMed=8696339;
Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalcman M.A., Koide H.B.,
Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
Vaillancourt J.P., Hayden M.R.;
"Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
is modulated by the polyglutamine tract";
Nat. Genet. 13:442-449(1996).
[12]
FUNCTION: Involved in the activation cascade of caspases
responsible for apoptosis execution. At the onset of apoptosis it
proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
element binding proteins (SREBPs) between the basic helix-loop-
helix leucine zipper domain and the membrane attachment domain.
Cleaves and activates caspase-6, -7 and -9. Involved in the
cleavage of huntingtin.
[13]
ENZYME REGULATION: Inhibited by isatin sulfonylamides.
[14]
SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
[15]
SUBCELLULAR LOCATION: Cytoplasmic.
[16]
TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
and kidney. Moderate levels in brain and skeletal muscle, and low
in testis. Also found in many cell lines, highest expression in
cells of the immune system.
[17]
PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
AND VICE VERSA.
[18]
SIMILARITY: Belongs to peptidase family C14.

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or send an email to license@isb-sib.ch).

EMBL; U13737; AAA65015.1; -
EMBL; U13738; AAA60355.1; -
EMBL; U26943; AAA74929.1; -

DR EMBL; AJ413269; CAC88866.1; -
DR EMBL; AY219866; AAO25654.1; -
DR EMBL; BC016926; AAH16926.1; -
DR PIR; A55315; A55315.
DR PDB; 1PAU; 07-JUL-97.
DR PDB; 1CP3; 24-DEC-97.
DR PDB; 1GFW; 23-JUN-00.
DR MEROPS; C14.003; -
DR Genew; HGNC:1504; CASP3.
DR MIM; 60636; -
DR GO; GO:0004208; F:caspase-3 activity; TAS.
DR GO; GO:000624; P:induction of apoptosis by extracellular sig.; TAS.
DR GO; GO:000829; P:induction of apoptosis by intracellular sig.; TAS.
DR GO; GO:000829; P:induction of apoptosis by intracellular sig.; TAS.
DR GO; GO:000829; P:induction of apoptosis by intracellular sig.; TAS.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR002138; ICE_P10.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENTZYM.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
3D-structure. 1 9
PROPEP 10 28
PROPEP 10 28
CHAIN 29 175
CHAIN 176 277
ACT SITE 121 121
ACT SITE 163 163
VARIANT 190 190
CONFLICT 31 36
STRAND 36 36
STRAND 43 51
HELIX 57 59
TURN 60 60
TURN 65 66
TURN 67 80
HELIX 81 82
TURN 81 82
Query Match 22.0%; Score 272.5; DB 1; Length 277;
Best Local Similarity 31.3%; Pred. No. 8.7e-15;
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;
QY 9 EEKYDMSGAALALILCVTK-----AREGSBEDLDALHMFQRLRFSTMKRDPTA 58
DB 34 DNSTYMDYPENGLCIINNNKFNFKSTGTSRGTDVAANLETRNLKYEVNKNLDR 93
QY 59 EFOFEELEKFOQAIIDSRDPVSCAFVLLMAHREGFLKGEDG--EMVKLENLFEALNNKN 116
DB 94 BEIVELMRDVSKEHDSKRSFVC---VLLSHGEFGIIFGTNGFVLDLKKITNFF---RGDR 147
QY 117 QOALRAKPKYIIOACRGQRDPG-ETVCGDEIVVMVKDSPTIPTYTDALHVTSTVEGY 175
DB 148 CRSTGPKPKFIIOACRGTELDGCIITDSGVDDVAC----HKIPVDADFLYATAGY 203
QY 176 IAYRHDKGSCFIQTLVDVFTK--RKGHILELLTEVTRMA-EAEIVQ---EGKARKNPP 229
DB 204 YSWNSKDGSGWFCISLCAMLKQVADKLEFNMHLTRVNRKVATEFESFSDATFHAKQTP 263
QY 230 EIQTILKRLY 240
DB 264 CIVSMLTKELY 274
RESULT 10
ICE7 MOUSE
ID ICE7_MOUSE STANDARD; PRT; 303 AA.
AC P97864; O08669;
DT 01-NOV-1997 (Rel. 35, Created)

1 01-NOV-1997 (Rel. 35, Last sequence update)
 2 10-OCT-2003 (Rel. 42, Last annotation update)
 3 Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
 4 protease Mch-3).
 5 CASP7 OR MCH3 OR LICE2.
 6 Mus musculus (Mouse).
 7 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 8 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 9 MCB_TaxID=10090;
 10 [1]
 11 SEQUENCE FROM N.A.
 12 TISSUE=Skeletal muscle;
 13 MEDLINE=97224489; PubMed=9070923;
 14 Juan T.S.-C., McNelece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 15 Copeland N.G., Fletcher F.A.,
 16 Identification and mapping of Casp7, a cysteine protease resembling
 17 CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 18 Genomics 40:86-93(1997).
 19 [2]
 20 SEQUENCE FROM N.A.
 21 MEDLINE=97236307; PubMed=9125129;
 22 Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
 23 Momoi T.;
 24 "Wormamin enhances CPP32-like activity during neuronal
 25 differentiation of P19 embryonal carcinoma cells induced by retinoic
 26 acid.";
 27 Biochem. Biophys. Res. Commun. 232:192-197(1997).
 28 [3]
 29 SEQUENCE FROM N.A.
 30 STRAIN=C3H/An;
 31 MEDLINE=97190206; PubMed=9038361;
 32 van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
 33 van de Craen M., Moelens P., Schotte P., van Crielinge W., Beyaert R.,
 34 Fiers W.;
 35 "Characterization of seven murine caspase family members.";
 36 FEBS Lett. 403:61-69(1997).
 37 [4]
 38 SEQUENCE FROM N.A.
 39 MEDLINE=2238257; PubMed=12477932;
 40 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 41 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 42 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 43 Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 44 Diatchenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,
 45 Stapleton M., Soares M.B., Bonaldo A.P., Casavant T.L., Scheetz T.E.,
 46 Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mungall A.J.,
 47 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 48 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 49 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 50 Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 51 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 52 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 53 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 54 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 55 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 56 "Generation and initial analysis of more than 15,000 full-length
 57 human and mouse cDNA sequences.";
 58 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 59 [1- FUNCTION: Involved in the activation cascade of caspases
 60 responsible for apoptosis execution. Cleaves and activates sterol
 61 regulatory element binding proteins (SREBPs). Overexpression
 62 promotes programmed cell death (By similarity).
 63 [1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
 64 [1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
 65 KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
 66 EXPRESSION IN THE BRAIN.
 67 [1- PM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 68 SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 69 CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 70 CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 71 VICE VERSA (BY SIMILARITY).
 72 [1- SIMILARITY: Belongs to peptidase family C14.
 73 This SWISS-PROT entry is copyright. It is produced through a collaboration
 74 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 75 the European Bioinformatics Institute. There are no restrictions on its
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 79 or send an email to license@isb-sib.ch).
 80 [1]
 81 EMBL; U67321; AAC53068.1; ALT_INIT.
 82 EMBL; D86353; BAA19730.1; --
 83 EMBL; Y13088; CAA73530.1; --
 84 EMBL; BC005428; AAH05428.1; --
 85 HSSP; P42574; 1PAU.
 86 MEROPS; C14.004; --
 87 MGD; MGI:109383; Casp7.
 88 InterPro; IPR002138; ICE_P10.
 89 InterPro; IPR001309; ICE_P20.
 90 InterPro; IPR002398; Peptidase_C14.
 91 Pfam; PF00656; Peptidase_C14; 1.
 92 PRINTS; PRO0376; ILIBCEZYNE.
 93 SMART; SM00115; CASC; 1.
 94 PROSITE; PS01122; CASPASE_CYS; 1.
 95 PROSITE; PS01121; CASPASE_HIS; 1.
 96 PROSITE; PS02027; CASPASE_P10; 1.
 97 PROSITE; PS02026; CASPASE_P20; 1.
 98 Hydroxylase; Thiol protease; Zymogen; Apoptosis.
 99 FT PROPEP 1 23
 100 FT CHAIN 24 198
 101 FT PROPEP 199 206
 102 FT CHAIN 207 303
 103 FT ACT_SITE 144 144
 104 FT ACT_SITE 186 186
 105 FT CONFLICT 10 11
 106 FT CONFLICT 45 45
 107 FT CONFLICT 48 49
 108 SQ SEQUENCE 303 AA; 34060 MW; 747787B5B5F744 CRC64;
 109 Query Match 21.8%; Score 270; DB 1; Length 303;
 110 Best Local Similarity 32.6%; Pred. No. 1.5e-14;
 111 Matches 71; Conservative 36; Mismatches 101; Indels 10; Gaps 4;
 112 QY 29 REGSEEDLDALHMFRLPSTMKRDPPTABQFOEELKFKQQAIDSRDPSVCAVVLMA 88
 113 Db 87 RRGTKDAGALFKCFQNLGFVTVHNDSCAKMDLLRKASEEDHSNS---ACFACVLLS 143
 114 QY 89 HGREGLKGEDGEMVKLENFEALNNKNCQALRAKPKVILIQACRGQRDPGETVGDEI 148
 115 Db 144 HGEEDLIYKGG-VTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDGQADSGPI 202
 116 QY 149 VMVVKDSPTIPTYTDALHVTSTVEGYIARHDKGSCFIQTLVDVFTK--RKGHILELL 206
 117 Db 203 NIDANPRNKIPVEADFLFAYSTVPGYVWENPGKSGFWFQALCSILNHRGKDLINQIL 262
 118 QY 207 TVETRRMAEELVQEGKAR-----KTNPEIQSTLRKLY 240
 119 Db 263 TRVNDRVARHFESQSDDPFRFNEKKQIPCMVSMLTKEYL 300
 120 RESULT 11
 121 ICE7_MESAU
 122 ID ICE7_MESAU STANDARD; PRT; 303 AA.
 123 AC P55214;
 124 DT 01-OCT-1996 (Rel. 34, Created)
 125 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 126 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 127 DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
 128 DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
 129 DE (SCA-2).
 130 GN CASP7 OR MCH3.
 131 OS Mesocricetus auratus (Golden hamster).
 132 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
NCBI_TaxID=10036;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=SYRIAN; TISSUE=Liver;
MEDLINE=96224303; PubMed=8643593;
Pai J.-T., Brown M.S., Goldstein J.L.;
"Purification and cDNA cloning of a second apoptosis-related cysteine
protease that cleaves and activates sterol regulatory element binding
proteins.";
Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
C -i- FUNCTION: Involved in the activation cascade of caspases
responsible for apoptosis execution. Cleaves and activates sterol
regulatory element binding proteins (SREBPs). Proteolytically
cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
bond. Overexpression promotes programmed cell death (by
similarity).
C -i- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
(BY similarity).
C -i- SUBCELLULAR LOCATION: Cytoplasmic.
C -i- PM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
VICE VERSA (BY SIMILARITY).
C -i- SIMILARITY: Belongs to peptidase family C14.

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EMBL: U47332; AAC52595.1; --
HSSP: P42574; 1PAU.
MEROPS: C14.004; --
InterPro: IPR002138; ICE_p10.
InterPro: IPR001309; ICE_p20.
InterPro: IPR002398; Peptidase C14.
Pfam: PF00656; Peptidase C14; 1.
PRINTS: PR00376; ILIBENZME.
SMART: SM00115; CASC; 1.
PROSITE: PS01122; CASPASE_CYS; 1.
PROSITE: PS01121; CASPASE_HIS; 1.
PROSITE: PS0207; CASPASE_P10; 1.
PROSITE: PS0208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Zymogen; Apoptosis.
PROPEP 1 23 CASPASE-7 SUBUNIT P20.
CHAIN 24 198 BY SIMILARITY.
PROPEP 199 206 CASPASE-7 SUBUNIT P11.
CHAIN 207 303 BY SIMILARITY.
ACT SITE 144 144 BY SIMILARITY.
ACT SITE 186 186 BY SIMILARITY.
SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;
Query March 21.08; Score 260; DB 1; Length 303;
Best Local Similarity 31.74; Pred. No. 9.8e-14;
Matches 69; Conservative 39; Mismatches 100; Indels 10; Gaps 5;
29 REGSEEDLDAEHFRQLRPESTMKRDPTAEQFQEELEKFOQAIDSREDPVSCAFVILMA 88
87 RGTGDKDAEALFKFRSLGDFVVYVNDSCAKQDLLRKASEBDHNS--ACFACVLLS 143
89 HGRGFLKGEDEMGVLENLFEALNNKNCALAKPKVYIIQACRQEPDGTGSGDEI 148
144 HGEENLYKDGQ-VTPKILTAHFRGDRCKTLLKPKLFFIQACRGTLEDLDGQVADSGPI 202
149 VMWIKDSQTIPTVTDALHYSTVEGVIAVRHPQKSGKSCFTQTLVDVFTK--RKHILELL 206
203 NETDANFRKLPVZADFLPAYSTVPGYVSNFGKGSFWFQALCSILDEHGKDLIMQL 262

QY 207 TEVTRMA--EALVQB-GKARKTNPEIOSTLRKLY 240
DB 263 TRVDRVARHFESQDDPCFNEKQIPCMVSMILKELY 300

RESULT 12
ICE7 HUMAN
ID ICE7 HUMAN STANDARD; PRT; 303 AA.
AC P55210; Q13364; Q96BA0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (CWH-1).
GN CASP7 OR MCH3
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plimates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=96139498; PubMed=8576161;
Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
Dixit V.M.;
RA "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
cell death protein Ced-3 is activated during fas- and tumor necrosis
factor-induced apoptosis.";
RT J. Biol. Chem. 271:1621-1625(1996).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX TISSUE=Spleen;
MEDLINE=9647144; PubMed=8567622;
Lippke J.A., Gu Y., Sarnecki C., Caron P.R., Su M.S.-S.;
RA "Identification and characterization of CPP32/Mch2 homolog 1, a novel
cysteine protease similar to CPP32.";
RT J. Biol. Chem. 271:1825-1828(1996).
RL [3]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX TISSUE=T-cell;
MEDLINE=96105019; PubMed=8521391;
Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salvesson G.,
Earnshaw W.C., Litwack G., Alnemri E.S.;
RA "Mch3, a novel human apoptotic cysteine protease highly related to
CPP32.";
RT Cancer Res. 55:6045-6052(1995).
RL [4]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
RX TISSUE=Fetal lung, and fetal spleen;
MEDLINE=97224489; PubMed=9070923;
Juan T.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
Copeland N.G., Fletcher F.A.;
RA "Identification and mapping of Casp7, a cysteine protease resembling
CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
RX Genomics 40:86-93(1997).
RL [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX TISSUE=Skin;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
Baba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

PROCESSING.

MEDLINE=96353838; PubMed=8755496; Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M., Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J., Litwack G., Alnemri E.S., "In vitro activation of CPP32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FAD-like domains," Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).

-!- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Cleaves and activates sterol regulatory element binding proteins (SREBPs). Proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217 bond. Overexpression promotes programmed cell death.

-!- ENZYME REGULATION: Inhibited by isatin sulfonamides.

-!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3; Name=Alpha; IsoId=PS5210-1; Sequence=Displayed; Name=Beta; IsoId=PS5210-2; Sequence=VSP 000807; Note=Not proteolytically active; Name=Alpha'; Synonyms=Beta; IsoId=PS5210-3; Sequence=VSP 000806; Note=What we call isoform Alpha' is known in Ref.4 as Beta;

-!- TISSUE SPECIFICITY: Highly expressed in lung, skeletal muscle, liver, kidney, spleen and heart, and moderately in testis. No expression in the brain.

-!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR

VICE VERSA

-!- SIMILARITY: Belongs to peptidase family C14.

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EMBL; U95613; AAC50346.1; -
EMBL; U40281; AAC50352.1; -
EMBL; U37448; AAC50303.1; -
EMBL; U37449; AAC50304.1; -
EMBL; U67319; AAC51152.1; -
EMBL; U67320; AAC51153.1; -
EMBL; U67206; AAF2460.1; -
EMBL; BC015799; AAH15799.1; -
PDB; 1FLJ; 23-MAY-01.
PDB; 1GQF; 04-JAN-02.
PDB; 1I40; 31-OCT-01.
PDB; 1I51; 23-FEB-02.
PDB; 1K86; 21-NOV-01.
PDB; 1K88; 21-NOV-01.
PDB; 1KMC; 16-JAN-02.
MEROPS; C14.004; -
Genew; HGNC:1508; CASP7.
MIM; 601761; -
GO; GO:0005737; Cytoplasm; TAS.
GO; GO:0008234; F:cysteine-type peptidase activity; TAS.
GO; GO:0008632; P:apoptotic program; TAS.

DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002396; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PRO0376; IILBENZYM.
DR SMART; SMO0115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
KW Hydrolase; thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW 3D-structure.
FT PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186
FT VARSPLIC 1 1
FT VARSPLIC 149 303
FT VARSPLIC 149 303
FT MUTAGEN 186 186
FT CONFLICT 4 4
FT CONFLICT 194 194
FT SEQUENCE 303 AA; 34276 MW; CD373EE54A232CA4 CRC64;
Query Match 20.7%; Score 256; DB 1; Length 303;
Best Local Similarity 30.7%; Pred. No. 2e-13;
Matches 67; Conservative 39; Mismatches 102; Indels 10; Gaps 4;
QY 29 REGSEEDDALEHMFROQLRSTWKRPTAEQFOEELEKFOQAIQDSREDVSCAFVVLMA 88
DB 87 RGTGDKDAELFKCFRSLGDFVIVINDCSAKQDLLK--ASEEDHTNAACFACILLS 143
QY 89 HGREGLKGEDGEMVKLENLEALNNKNCQALRAKPKVYIQACRGEQRDPGTGVDGI 148
DB 144 HGEENVYKDG-VTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDGIGADSGPI 202
QY 149 VMVVKDSQTTPTVTDALHYVTVGVIAYEHDKGSCFTQTLVDVFTK--RKGHILELL 206
DB 203 NDTDANPKYKIPVEADFLFAYSTVPGYISWRSPGWSFWQALCSILEEHGKLEINQIIL 262
QY 207 TEVTRMAEALVQBG----KARKTNPSIQSTLRKRLY 240
DB 263 TVNDRVARHFTESQSDPHFHEKQIPCVWSMLTKELY 300
RESULT 13
CED3_CABEL STANDARD; PRT; 503 AA.
ID CED3_CABEL
AC P42573; P45435; Q9G004; Q9NAQ8;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cell death protein 3 precursor (EC 3.4.22.-).
GN CED-3 OR C48D1.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC STRAIN=Bristol N2;
RX MEDLINE=94061982; PubMed=8242740;
RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;

A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lei Z.,
A Lesko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
A Liu K., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
A Palazolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamis I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
I "The genome sequence of Drosophila melanogaster."
L Science 287:2185-2195 (2000).
[3]
P SEQUENCE FROM N.A.
C STRAIN=Berkeley; TISSUE=Head;
C MEDLINE=22426066; PubMed=12537569;
X A Stapleton M., Carlson J.W., Brakstein P., Yu C., Champe M.,
A George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
A Rubin G.M., Celnik S.E.,
T "A Drosophila full-length cDNA resource."
L Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
C C -i- FUNCTION: Involved in the activation cascade of caspases
C responsible for apoptosis execution. Acts downstream of rpr.
C cleaves baculovirus p35 and lamin Dmo in vitro.
C -i- SUBUNIT: Heterodimer of a 21 kDa (p21) and a 12 kDa (p12) subunit.
C -i- DEVELOPMENTAL STAGE: Expressed at all stages where apoptosis
C occurs.
C -i- SIMILARITY: Belongs to peptidase family C14.
C -----
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C between the Swiss Institute of Bioinformatics and the EMBL outstation -
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C entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
C or send an email to license@isb-sib.ch).
C -----
C EMBL; Y12261; CAA72937.1; --
C EMBL; AE003771; AAF56339.1; --
C EMBL; AY058451; AAL13680.1; --
C HSSP; P42574; 1PAU.
C MEROPS; C14.015; --
C FlyBase; FBgn0019972; Ice.
C GO; GO:0004207; P:effector caspase activity; NAS.
C GO; GO:0006915; P:apoptosis; NAS.
C InterPro; IPR002138; ICE_p10.
C InterPro; IPR001309; ICE_p20.
C InterPro; IPR002398; Peptidase C14.
C Pfam; PF00656; Peptidase C14; 1.
C PRINTS; PR00376; IILBCEZYME.
C SMART; SM00115; CASc; 1.
C PROSITE; PS01122; CASPASE_CYS; 1.
C PROSITE; PS01122; CASPASE_HIS; 1.
C PROSITE; PS02070; CASPASE_F10; 1.
C PROSITE; PS02080; CASPASE_P20; 1.
C Hydrolase; Thiol protease; Zymogen; Apoptosis.
C PROPEP 1 28 BY SIMILARITY.
C CHAIN 29 217 CASPASE SUBUNIT P21 (BY SIMILARITY).
C CHAIN 218 230 BY SIMILARITY.
C PROPEP 231 339 CASPASE SUBUNIT P12 (BY SIMILARITY).
C ACT_SITE 169 169 BY SIMILARITY.
C ACT_SITE 211 211 BY SIMILARITY.
C CONFLICT 151 151 A -> S (IN REF. 1).
C CONFLICT 265 265 S -> T (IN REF. 1).
C SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;
QY 27 KARGSSSEDLDALHEMFROLRFESTMKRDPATAFQOBELEKFOCAIDSRDPVSCAFVVL 86
DB 110 KSRAGTNVDCNLTURLKQDFFETVTKDC--YYKDLILTEYAAASQNSHSDCILVAI 166
QY 87 MAHGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGQRDPGETV--- 143
DB 167 LSHGEMGIYAKDTQ-YKLDNINWFFFTANHCPSLAGPKLFFIQAQCGRLDGGVTMQRS 225
QY 144 ---GGDEINWIKDSQTTPTFYTDALHVTSTVEGYIAYEHDKGSCFICQLVDVFTK-- 197
DB 226 QETDGD-----SSMSYKIPVHADFLIAYSTVPGFYSWRNTTRGSWFMSQSLCAELAANG 279
QY 198 RKGHILELLTEVTERMA 214
DB 280 KELDILTLLTFVCORVA 296
RESULT 15
ICB8 HUMAN STANDARD; PRT; 479 AA.
ID IC88 HUMAN STANDARD; PRT; 479 AA.
AC Q14790; Q14676; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796;
AC Q15780; Q15806; Q8TD11; Q8TD12; Q8TD13; Q8TD14; Q8TD15; Q8TD22;
AC Q9COK4; Q9UQ8.;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
DE (Apoptotic protease Mch-5) (CAP4).
GN CASP8 OR MCH5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 5; 6; 7 AND 8).
RC TISSUE=B-cell and Thymus;
RX MEDLINE=96279826; PubMed=8681376;
RA Boldin M.P., Goncharov T.M., Goitsev Y.V., Wallach D.;
RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
RL Fas/APO-1- and TNF receptor-induced cell death.";
RL Cell 85:803-815 (1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX MEDLINE=96279827; PubMed=8681377;
RA Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
RA Kramer P.H., Peter M.E., Dixit V.M.;
RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
RL to the CD95 (Fas/APO-1) death-inducing signaling complex.";
RL Cell 85:1817-827 (1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RL apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132295; PubMed=9931493;
RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
RT "Structure and chromosome localization of the human CASP8 gene.";
RL Gene 226:225-232 (1999).

- [5] SEQUENCE FROM N.A. (ISOFORM 2).
P MEDLINE=97373543; PubMed=9228018;
X A Srinivasula S.M., Ahmad M., Otilie S., Bullrich F., Banks S.,
A Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
A Armstrong R.C., Alnemri E.S.;
T "FLAME-1, a novel PADD-like anti-apoptotic molecule that regulates
L Fas/TNFR1-induced apoptosis";
L J. Biol. Chem. 272:18542-18545 (1997).
[6] SEQUENCE FROM N.A.
P MEDLINE=21100893; PubMed=11161814;
X A Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
P Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
A Ikeda J.-E., Hayden M.R.;
T "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
T and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2),
T critical region at chromosome 2q33-q34: candidate genes for ALS2";
L Genomics 71:200-213 (2001).
[7] SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
P TISSUE=Leukocyte;
P MEDLINE=22005982; PubMed=12010809;
X A Hameji D., Horuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
A Harada M.;
T "Characterization of caspase-8L: a novel isoform of caspase-8 that
T behaves as an inhibitor of the caspase cascade";
L Blood 99:4070-4078 (2002).
[8] SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM 9
P WITH SCAP31 AT THE ENDOPLASMIC RETICULUM.
X MEDLINE=21927603; PubMed=11917123;
P Breckenridge D.G., Nguyen M., Kupzig S., Reth M., Shore G.C.;
X "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
T complex at the endoplasmic reticulum";
L Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336 (2002).
[9] SEQUENCE FROM N.A. (ISOFORM 7).
P TISSUE=Leukocyte;
X MEDLINE=22388257; PubMed=12477932;
P Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
X Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
X Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
X Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
X Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
X Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Kryzinski M.I., Skalka U., Smailus D.E.,
X Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length
T human and mouse cDNA sequences";
L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[10] PARTIAL SEQUENCE, AND PROCESSING.
X MEDLINE=97121412; PubMed=8962078;
X Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
A Alnemri E.S.;
T "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
T protease Mch5 is a CrmA-inhibitable protease that activates multiple
T Ced-3/ICE-like cysteine proteases";
L Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
[11] FUNCTION.
X MEDLINE=97160607; PubMed=9006941;
X Muzio N., Salvesen G.S., Dixit V.M.;
T "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
T zymogens";
L J. Biol. Chem. 272:2952-2956 (1997).
[12] PROCESSING.
X MEDLINE=97327557; PubMed=9184224;
X Medema J.P., Scalfi C., Kischkel F.C., Shevchenko A., Mann M.,
A Krammer P.H., Peter M.E.;
T "FLICE is activated by association with the CD95 death-inducing
T signaling complex (DISC)";
L EMBO J. 16:2794-2804 (1997).
[13] CHARACTERIZATION OF ISOFORM 7.
X MEDLINE=20318377; PubMed=10860845;
X Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
A Hayashi K.;
T "Dominant expression of a novel splice variant of caspase-8 in human
T peripheral blood lymphocytes";
L Biochem. Biophys. Res. Commun. 272:877-881 (2000).
[14] INTERACTION WITH BCL2; BCL2L1 AND BCAP31.
X MEDLINE=97477382; PubMed=9334338;
X Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
A Cromlish J.A., Shore G.C.;
T "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
T endoplasmic reticulum";
L J. Cell Biol. 139:327-338 (1997).
[15] INTERACTION WITH PEAL5.
X MEDLINE=99369240; PubMed=10442631;
X Condorelli G., Vigliotta G., Caffieri A., Trecia A., Andalo P.,
A Oriente F., Miele C., Caruso M., Formisano P., Beguinot P.;
T "FED/PEA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
T induced apoptosis";
L Oncogene 18:4409-4415 (1999).
[16] X-RAY CRYSTALLOGRAPHY (2.8 ÅNGSTRÖMS).
X MEDLINE=99451259; PubMed=10508784;
X Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
A Wu J.C., Tonaselli K.J., Gruetter M.G.;
T "The three-dimensional structure of caspase-8: an initiator enzyme in
T apoptosis";
L Structure 7:1125-1133 (1999).
[17] VARIANT CASP8 TRP-248.
X MEDLINE=22399940; PubMed=12353035;
X Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
A Dale J.K., Fack J., Davis J., Hall C.G., Skoda-Smith S.,
X Atkinson T.P., Straus S.B., Lenardo M.J.;
T "Pleiotropic defects in lymphocyte activation caused by caspase-8
T mutations lead to human immunodeficiency";
L Nature 419:395-399 (2002).
-!- FUNCTION: Most upstream protease of the activation cascade of
C caspases responsible for the TNFRSF6/Fas mediated and TNFRSF1A
C induced cell death. Binding to the adapter molecule PADD recruits
C it to either receptor. The resulting aggregate called death-
C inducing signaling complex (DISC) performs CASP8 proteolytic
C activation. The active dimeric enzyme is then liberated from the
C DISC and free to activate downstream apoptotic proteases.
C Proteolytic fragments of the N-terminal propeptide (termed CAP3,
C CAP5 and CAP6) are likely retained in the DISC. Cleaves and
C activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
C participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
C Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
C Likely target for the cowpox virus CRMA death inhibitory protein.
C Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
C with the pro-apoptotic activity of the complex.
-!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
C Interacts with FADD, CFLAR and PEAL5. Isoform 9 interacts at the
C endoplasmic reticulum with a complex containing BCAP31, BAP29,
C BCL2 and/or BCL2L1.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:

```

Event=Alternative splicing; Named isoforms=9;
Name=1; Synonyms=Alpha-1;
ISOID=Q14790-1; Sequence=Displayed;
Name=2; Synonyms=Alpha-2, MCH5-beta;
ISOID=Q14790-2; Sequence=VSP_000810;

Query Match      19.9%; Score 246.5; DB 1; Length 479;
Best Local Similarity 29.7%; Pred No. 2,1e-12;
Matches 80; Conservative 37; Mismatches 115; Indels 37; Gaps 9;

Y 3 NPRSLEEK-----YDMGALALILCV-----TKARE-----GSEEDLDAL 39
C 211 SPREQDSEQTLDKVYQMKSPRGYCLIIINNHNFAKAREKVPKLHSIRDRNGTHLDAGAL 270
Y 40 EHMFCRLREESTMKDPTAEQFOEELKFOQAIDSRDPVSCAFVWLMARGEGFLKGED 99
b 271 TTTFEELHFEIKPHDDCTVEQIYEILKIYQLMDHSNMD---CFICCLSHGDKGIYGTD 327
Y 100 GEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDRDPGETVGGDE---IVMVIKDS 155
b 328 GQEAPIVELTSQFTGLKCPSLAGKPKVFFIQACQGDNYQKGIPIVETDSEEQPYLEMDLSS 387
Y 156 PQT--IPTYTDALHYVSTVEGYIAYEHQKGSCTIQTLDVDFTKR--KG-HILELLTEVT 210
b 388 PQTRYIPDEADFLGMATVNNCVSTNPAEGTWIQLCSLRERCPRGDDILTILTEVN 447
Y 211 RMAEAELVQEGKARKTNPEIQSTLRKEL 239
b 448 YEVSNKD--DKKMGKQMPQPTFTLRKKL 474
```

Search completed: March 19, 2004, 11:22:46
Job time : 10.6414 secs

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WM protein - protein search, using sw model

run on: March 19, 2004, 11:18:31 ; Search time 13.498 Seconds
(without alignments)
1724.577 Million cell updates/sec

title: US-09-989-903-5
perfect score: 1239
sequence: 1 MSNPRSLSEEEKYDMSGALAL.....KARKTNPEIQSTLRRLYLQ 242

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	2 JC7517	caspase-14/a - human
2	293	23.6	452	2 JC6507	caspase-2 - rat
3	289	23.3	435	2 A54821	apoptosis regulato
4	282.5	22.8	277	2 JC5410	CPP32 protein - mo
5	280.5	22.6	277	2 S64710	cysteine proteinas
6	272.5	22.0	277	2 A53315	cysteine proteinas
7	264.5	21.3	454	2 JC7123	caspase-9 long cha
8	248.5	20.1	503	2 A49429	interleukin-1 beta
9	246.5	19.9	212	2 I67437	cysteine proteinas
10	239.5	19.3	416	2 G02635	ICE-LAP6 - human
11	230	18.6	495	2 T20038	hypothetical prote
12	226	18.2	311	2 B56084	interleukin-1 beta
13	226	18.2	383	2 A56084	interleukin-1 beta
14	226	18.2	404	2 A26777	interleukin-1 beta
15	225	18.2	418	2 B57511	interleukin-1 beta
16	217.5	17.6	402	2 A46495	IL-1 beta converta
17	213.5	17.2	182	2 I67436	interleukin-1-beta
18	210.5	17.0	826	2 T43638	caspase-related pr
19	207	16.7	263	2 C56084	interleukin-1 beta
20	205.5	16.6	377	2 A57511	interleukin-1 beta
21	197	15.9	312	2 B54821	apoptosis regulato
22	189	15.3	536	2 T43633	caspase-related pr
23	185	14.9	488	2 T13385	hypothetical prote
24	174.5	14.1	642	2 T27021	hypothetical prote
25	159.5	12.9	136	2 I53300	interleukin-1-beta
26	103.5	8.4	1313	2 A48467	myosin heavy chain
27	98	7.9	1357	2 A45627	caspase protein 3
28	97.5	7.9	139	2 T43642	caspase protein 3
29	97	7.8	1051	2 T18302	apsB protein - Eme

30 95.5 7.7 1190 2 E84193 chromosome segrega
31 95.5 7.7 2104 2 T38774 myosin-3 heavy cha
32 95 7.7 761 2 E82205 chemotaxis protein
33 91 7.3 394 2 T25968 hypothetical prote
34 91 7.3 510 2 S42626 ER-golgi intermedi
35 90.5 7.3 520 2 F70350 recombination prot
36 89.5 7.2 467 2 D95253 L-fucose kinase
37 89.5 7.2 482 2 B98118 rhamnulokinase (EC
38 89.5 7.2 1225 2 A56514 chromokinesin - ch
39 89 7.2 352 2 G71328 probable flagellar
40 88.5 7.1 149 2 T43637 caspase protein 1C
41 88.5 7.1 661 2 B97733 excinuclease ABC s
42 88.5 7.1 858 1 IJRTNC neural cell adhesi
43 88.5 7.1 1203 2 B55094 chromosomal protei
44 88.5 7.1 2954 2 T14156 kinesin-related pr
45 88 7.1 505 2 S39520 H+-transporting tw

ALIGNMENTS

RESULT 1

JC7517
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7517
R:Beckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.
Biochem. Biophys. Res. Commun. 277, 655-659, 2000
A:Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyte
A:Reference number: JC7517; MUID:20517231; PMID:11062009
A:Contents: Epidermal keratinocytes
A:Accession: JC7517
A:Molecule type: mRNA
A:Residues: 1-242 <ECK>
A:Cross-references: GB:AF097874
C:Comment: This enzyme accumulates during keratinocyte differentiation and is activated
C:Genetics:
A:Gene: casp-14/a
A:Map position: 19p13.1
A:Introns: 9/3; 59/3; 135/1; 174/1; 208/3
C:Keywords: differentiation

Query Match 99.6%; Score 1234; DB 2; Length 242;
Best Local Similarity 99.6%; Pred. No. 1.2e-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRFESTWKRDPDTAQ 60
Db 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTWKRDPDTAQ 60
QY 61 FOEELKFOQAIDSREDPVSCAFVLMHAGREGFLKGDGEVWKLNLFEALNNKNCQAL 120
Db 61 FOEELKFOQAIDSREDPVSCAFVLMHAGREGFLKGDGEVWKLNLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQDPGTGGDSIVNVVVKDSPTIPTTYTDALHVTSTVEGYAYRH 180
Db 121 RAKPKVYIIQACRGQDPGTGGDSIVNVVVKDSPTIPTTYTDALHVTSTVEGYAYRH 180
QY 181 DQKSGCFIQTLLVDVFTTKRGHILELLTEVTRMAEALVOEGKARKTNPEIQSTLRKLY 240
Db 181 DQKSGCFIQTLLVDVFTTKRGHILELLTEVTRMAEALVOEGKARKTNPEIQSTLRKLY 240
QY 241 LQ 242
Db 241 LQ 242

RESULT 2

JC6507
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000


```
;Accession: JC6507
;Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
;Date: 127-132, 1997
;Title: Cloning and expression of the cDNA encoding rat caspase-2.
;Reference number: JC6507; MUID:98087427; PMID:9427555
;Accession: JC6507
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-452 <SAT>
;Cross-references: GB:U77933; NID:g2769705; PIDN:AAB96379.1; PID:g2769706

Query Match      23.6%; Score 293; DB 2; Length 452;
Best Local Similarity 31.5%; Pred. No. 3e-15; Indels 36; Gaps 7;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Y 29 REGSEEDLDALHMFRLQFESTMKRDPPTAEQFQEELEKFOQAIDSRDPVSCAFVILMA 88
b 219 RSGGDVHTTLVTLFKLLGVNVHVLVDQTAQEMQEKLNFAQ-LPAHRVTDSC-IVALLS 276
Y 89 HGREGLKGEDGMVKLENLFEALNNKCOALRAKPKVYIIQACRGEQDPG----- 140
b 277 HGVEGGIYGVGKLLQQLQVFLFDNANCPSLQNKPKMFFQACRGDETDGVDVQDGKN 336
Y 141 -----ETVGGDEIVMWIKDSPQTIPTTIDALHYSTVEGYIAYRHDKGSCFIOTLV 192
b 337 HAQSPGCEESDAGKEELMKVR-----LPTSDMIGYACLGKNAAMRNKRGSWYIEALT 391
Y 193 DVFTKR--KGHILELLETVTRMAEELVQEGKARKTN-----PEIQTSLRKRLYL 241
b 392 QVFSEACDMHVDMLVKVNALIKE----REGVAPGTEPHRCCKEMSEYCSILCOOLYL 445

RESULT 3
154821
;Species: Homo sapiens (man)
;Title: Ich-1, a stimulatory form L - human
;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
;Accession: A54821
;Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
;Cell 78, 739-750, 1994
;Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
;Reference number: A54821; MUID:94373811; PMID:8067842
;Accession: A54821
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-435 <WAN>
;Cross-references: GB:U13021; NID:g537291; PID:g537292
;Keywords: alternative splicing; apoptosis

Query Match      23.3%; Score 289; DB 2; Length 435;
Best Local Similarity 31.1%; Pred. No. 5.9e-15; Indels 36; Gaps 7;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

Y 29 REGSEEDLDALHMFRLQFESTMKRDPPTAEQFQEELEKFOQAIDSRDPVSCAFVILMA 88
b 202 RSGGDVHSTLVTFLKLLGVNVHVLVDQTAQEMQEKLNFAQ-LPAHRVTDSC-IVALLS 259
Y 89 HGREGLKGEDGMVKLENLFEALNNKCOALRAKPKVYIIQACRGEQDPG----- 140
b 260 HGVEGGIYGVGKLLQQLQVFLFDNANCPSLQNKPKMFFQACRGDETDGVDVQDGKN 319
Y 141 -----ETVGGDEIVMWIKDSPQTIPTTIDALHYSTVEGYIAYRHDKGSCFIOTLV 192
b 320 HAGSPGCEESDAGKE-----KLQWRLPTRSDMTCGVACLGKGTAAAMNTRKGSWYIEALA 374
Y 193 DVFTKR--KGHILELLETVTRMAEELVQEGKARKTN-----PEIQTSLRKRLYL 241
b 375 QVFSEACDMHVDMLVKVNALIKD----REGVAPGTEPHRCCKEMSEYCSILCRHLYL 428

RESULT 4
JC5410
-PP32 protein - mouse

;Species: Mus musculus (house mouse)
;CDate: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
;Accession: JC5410
;Mukasa, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
;Biochem. Biophys. Res. Commun. 231, 770-774, 1997
;Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation
;Reference number: JC5410; MUID:97224429; PMID:9070890
;Accession: JC5410
;A:Status: nucleic acid sequence not shown
;Molecule type: mRNA
;Residues: 1-277 <MUK>
;Cross-references: DDBJ:D86352
;Experimental source: embryo
;Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match      22.8%; Score 282.5; DB 2; Length 277;
Best Local Similarity 32.4%; Pred. No. 1.1e-14; Indels 27; Gaps 8;
Matches 81; Conservative 38; Mismatches 104; Indels 27; Gaps 8;

Y 9 EBYDMSGAALALILCVT-----KAREGSEEDLDALHMFRLQFESTMKRDPPTA 58
b 34 DSSYKWDYPENGICIIITINKNFHKSCTGWSRSRSGTDVAANLRETFMGLKYEVNRKNDLTR 93
Y 59 EQFQEELEKFOQAIDSRDPVSCAFVILMAHGREGLKGEDGMVKLENLFEALNNKNCQ 118
b 94 EEIMELMDSVSKEDSHKSSPVC---VILSHGDEGVIFGNGP-VDLKLTSPFRGDYCR 149
Y 119 ALRAKPKVYIIQACRGEQDPG-ETVGGDEIVMWIKDSPQTIPTTIDALHYSTVEGYIA 177
b 150 SLTGKPKFLIIQACRGTELDGCIETDSTDEMAC---QKIPVEADFLVAYSTAPGYS 205
Y 178 YRHDKGSCFIOTLVDTVKRKHILE---LLTEVTRMA-----EALVQEGKARKTNPE 230
b 206 WRNSKDGSWFIQSLCSML-KLYAHKLEFHLTRVNRKVATEPESFSLDSTFFHAKKOIPC 264
Y 231 IOSTLRKRLYL 240
b 265 IVSMLTKELY 274

RESULT 5
S64710
cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
;Species: Cricetus griseus (Chinese hamster)
;CDate: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
;Accession: S64710; S72395
;Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
;EMBO J. 15, 1012-1020, 1996
;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
;Reference number: S64710; MUID:96183185; PMID:8605870
;Accession: S64710
;A:Status: nucleic acid sequence not shown
;Molecule type: mRNA
;Residues: 1-277 <WAN>
;Cross-references: EMBL:U27463
;Wang, X.
submitted to the EMBL Data Library, May 1995
;Accession: S72395
;Reference number: S72395
;Molecule type: mRNA
;Residues: 1-79, A, 81-146, Y, 148-277 <WAN>
;Cross-references: EMBL:U27463; NID:G1244443; PIDN:AAB01511.1; PID:G1244444
;Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match      22.6%; Score 280.5; DB 2; Length 277;
Best Local Similarity 35.9%; Pred. No. 1.6e-14; Indels 17; Gaps 7;
Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;

Y 29 REGSEEDLDALHMFRLQFESTMKRDPPTAEQFQEELEKFOQAIDSRDPVSCAFVILMA 88
b 64 RSGTDVDAAKLRETFMNLKYEVNRKNDLTRFEEIVELMKNKASDESHKSSPVC---VILS 120
Y 89 HGREGLKGEDGMVKLENLFEALNNKCOALRAKPKVYIIQACRGEQDPG-ETVGGDE 147
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121 HGDEGVFGTGGP-IDLKLTSTVFRGDRGRSLGKPKLFIQACRGTELDGCIETDSSTE 179
148 IVWIKDQSPQITTYTDALHVVSTVEGYIAYRHQKQSCFIQTLVDVFTPKRGHILE--- 204
180 DMTC-----QKIPVEADFLYAYSTAPGYYSWRNPKDGSFQISLCSML-KLYAHLKLEPMH 234
205 LLEVTFRMA-----EALVQEGKARKTNPEIQSTLRKRLY 240
235 ILTRVNRKVATEPESPSLDSSTFRHKKQIPICIVSMLTKELY 274

RESULT 6
55315
>Species: Homo sapiens (human)
>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
>Accession: A55315; S58899; I39005
>Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
>J. Biol. Chem. 269, 30761-30764, 1994
>Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
>Reference number: A55315; MUID:95074098; PMID:7983002
>Accession: A55315
>Status: preliminary
>Molecule type: mRNA
>Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666
>Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.
>Yu, V.L.; Miller, D.K.
>Nature 376, 37-43, 1995
>Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian
>apoptosis
>Reference number: S58899; MUID:95319529; PMID:7596430
>Accession: S58899
>Molecule type: protein
>Residues: 29-46; 176-189, 'E', 191-193 <NIC>
>Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier,
>Cell 81, 801-809, 1995
>Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
>Reference number: A56924; MUID:95292347; PMID:7774019
>Accession: I39005
>Status: preliminary
>Molecule type: mRNA
>Residues: 1-189, 'E', 191-277 <RES>
>Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569
>Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 22.0%; Score 272.5; DB 2; Length 277;
Best Local Similarity 31.9%; Pred. No. 6.5e-14;
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

2Y 9 EEKYDMGSAALALILCVTK-----AREGSEEDLDALHMFQRLRFESTMKRDPTA 58
2D DNSTKMDYPENGLCIIINRNFKHSTGTSRSGVDVDAANRLRTFNKLYEVNRKNDLTR 93
2Y 59 EQFOEELEKFOQAIDSDREDPVSCAFVYLMARHREGFLKSGEDG--EMVKLENLFEALNNKN 116
2D 94 EEIVELMRDVSKEHDHKSRSFVC---VLLSHGEGGIIFGTNGPVDLKKITNPF---RGDR 147
2Y 117 QALRAKPKVYIIQACRGEQDPG-ETVGGDEIVWVKDSQPQIPYTDALHVVSTVEGY 175
2D 148 CRSITGPKLFIQACRGTELDGCIETDSGVDDMAC-----HKIPVDVDFLYAYSTAPGY 203
2Y 176 IAYRHQKQSCFIQTLVDVFTK--RKGHILELLETVTRMA-EAELVQ---EGKARKTNP 229
2D 204 YSWNSKDGSGFQISLCSMLKQYADKLEFHWHLTVNRKVATEFESFSDATPHAKKQIP 263
2Y 230 EIQSTLRKRLY 240
2D 264 CIVSMLTKELY 274

RESULT 7

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JC7123

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caspase-9 long chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: JC7123
R;Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A;Reference number: JC7123; MUID:20001956; PMID:10529400
A;Accession: JC7123
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-454 <FUJ>
A;Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

```

Query Match 21.3%; Score 264.5; DB 2; Length 454;

Best Local Similarity 30.6%; Pred. No. 4.9e-13;

Matches 76; Conservative 36; Mismatches 89; Indels 47; Gaps 7;

QY 29 REGSEEDLDALHMFQRLRFESTMKRDPTAEQ-----FOBELEKFOQAIDSDREDPVSCAFV 84

DB 218 RTGNSNDRDKLEHRFELWLFPMVEVKNDLTAKQWVTALMEMAHRNHRALD-----CFVV 270

QY 85 VLMHGRE-----GFLKGEDGEMVKLENLFEALNNKNCOALRAKPKVYIIQACRGQR 137

DB 271 VILSHGCOASHLQFPQAVYGTGCSVIEKIVNIFNGSCPSLGGKPKLFIQACGGQK 330

QY 138 D-----PGETVGGDEIVWVK-----DSPQITPYTDALHVVSTVEGYI 176

DB 331 DHGFEVACTSSQGRITLSDSEDPATPFQEGPRPLDQLDAVSSLPTPSDILVSYSTFPQGV 390

QY 177 AYRHQKQSCFIQTLVDVFTK--RKGHILELLETVTRMAEALVQEGKARKTNPEIQST 234

DB 391 SWRDKSGSWGIETLGLILFQWARSDELQSLLRV-----ANAVSEKGVYKQIPGCFNF 444

QY 235 LRKRLYLQ 242

DB 445 LRKRLFFK 452

RESULT 8

```

A49429
interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C;Accession: A49429; T37312
R;Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
Cell 75, 641-652, 1993
A;Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int
A;Reference number: A49429; MUID:94061982; PMID:8242740
A;Accession: A49429
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-503 <YUA>
A;Cross-references: GB:L29052; NID:96503232; PIDN:AAA27982.2; PID:96503233
A;Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBI:139826)
A;Accession: T37312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-417, 'R', 419-503 <YU2>
A;Cross-references: EMBL:L29052; PIDN:AAA27982.1
C;Genetics:
A;Gene: ced-3
A;Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

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Query Match 20.1%; Score 248.5; DB 2; Length 503;

Best Local Similarity 27.9%; Pred. No. 9.8e-12;

Matches 68; Conservative 42; Mismatches 93; Indels 41; Gaps 6;

QY 29 REGSEEDLDALHMFQRLRFESTMKRDPTAEQBELEKFOQAIDSDREDPVSCAFVYLM 88

DB 259 RNGTKADKNDLTNLCRMGVTVICKNTLGRGMLLTIRDFAK----HESHGSDSAILVILS 314

89 HREGFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPGETV-----143
315 HGENVIIGVDIPISITHEIYDLNANAPRLANKPKIVFVQACRGERDNGFPVLDSVD 374
144 -----GGDEIWMVKDSP-----QTIPTTALHVSIVVEGYIAYR 179
375 GVPAFLRRGWN-----RDGFLNFGICVRPQVQVWRKKPQADILLAYATAQYVSWR 429
180 HDQKSGCFIQLVDVFT--KRGHILELLETVTRRMAEALVQEG-KARKTNPEIQSTLR 236
430 NSARGSWFIQAVCEVFSTHAKDMVDVVELLTVNKKVACGFTSQSNNILKOMPENTRELL 489
237 KRLY 240
490 KKFY 493
RESULT 9
67437
;Species: Rattus norvegicus (Norway rat)
;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
;Accession: I67437
;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.; Til
ndocrinology 136, 5042-5053, 1995
;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPe) and mammalian cel
ulosa cells of the ovarian follicle.
;Reference number: I53300; MUID:96042508; PMID:7588240
;Accession: I67437
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: mRNA
;Residues: 1-212 <RES>
;Cross-references: EMBL:U34685; NID:G1004370; PIDN:AAC52261.1; PID:G1004371
;Keywords: cysteine proteinase; hydrolase
Query Match 19.9%; Score 246.5; DB 2; Length 212;
Best Local Similarity 31.5%; Pred. No. 5e-12;
Matches 69; Conservative 34; Mismatches 89; Indels 27; Gaps 8;
Y 9 BEKDMGSAALALICVT-----KAREGSEDLDALEHMFQRLRFESTWKRPDTA 58
b 5 DSSYMDYEPENGLCIINNNFKHSGTGMARNGTVDAAANLRETFWALKYEVNRKNDLTR 64
Y 59 EQFOELEKFOQAIIDSDREDPVSCAFVLMAGHREGFLKGEDEGMVKLENLFEALNNKNCQ 118
b 65 EEIMELMDSVSKEDHKSRSFVC---VILSHGDEGVIFGTNGP-VDLKKLTSFFRGDYCR 120
Y 119 ALRAKPKVYIIQACRGEQDPG-ETVGG--DEIVMWIKDSPQTIPTTYTALHVSIVVEGY 175
b 121 SLTGKPKLFIQACRGTSLDSGIEISGADDDVAC-----QKKPEADFLYAYSSAPGY 174
Y 176 IAYRHDKGSCFIQTLVDVFTKRGHILELLETVTRRMAEALVQEG-KARKTNPEIQSTLR 211
b 175 YSWNSRGGSWFIQSLC-AMLKLYAHKLEFPMHILTRVNR 212
RESULT 10
102635
;Species: Homo sapiens (man)
;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
;Accession: G02635
;Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
submitted to the EMBL Data Library, April 1996
;Reference number: H01513
;Accession: G02635
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: mRNA
;Residues: 1-416 <DUA>
;Cross-references: EMBL:U56390; NID:G1336026; PIDN:AAC50640.1; PID:G1336027
Query Match 19.3%; Score 239.5; DB 2; Length 416;
Best Local Similarity 28.7%; Pred. No. 3.9e-11;

Matches 72; Conservative 46; Mismatches 84; Indels 49; Gaps 9;
QY 27 KAREGSEDLDALEHMFQRLRFESTWKRPDTAEOFOELEKFOQAIIDSDRED--PVSCAFV 84
Db 178 RTRGSGNIDCEKLARRRSSLHFVVEVKGDLTAKKMYLALLEL-----AQDHGALDCCVV 232
QY 85 VLMAGRE-----GFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQ 137
Db 233 VILSHGCOASHLOPPGAVYGTGCPVSEKIVNIFNGTSCPSLGGKPKLFFIQAACGGQK 292
QY 138 DPG-----ETVGG-----DEIVMWIKDSPQTIPTTYTALHVSIVVEGY 171
Db 293 DHGFEVASTSPEDSPGSPNPEPDATPFQEGRLTFDQ-----DAISSLTPSDIFVYST 347
QY 172 VEGYIAYRHDKGSCFIQTLVDVFTKRGHILELLETVTRRMAEALVQEGKARKTNPEI 231
Db 348 PFGFVSWRDPKSGSWYVETLDDIF-EGWAH-SSDQSLRLRVANAVSVK--GIYKQMPGC 403
QY 232 QSTLRKRIYLQ 242
Db 404 FNFELKKLFFK 414
RESULT 11
T20038
;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
;Accession: T20038
;Burton, J.
submitted to the EMBL Data Library, October 1996
;Reference number: Z19214
;Accession: T20038
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-495 <WIL>
;Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2
;Experimental source: clone C48D1
;Genetics:
;Gene: CESP:C48D1.2
;Map position: 4
;A: Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1
Query Match 18.6%; Score 230; DB 2; Length 495;
Best Local Similarity 27.6%; Pred. No. 2.6e-10;
Matches 60; Conservative 39; Mismatches 78; Indels 40; Gaps 5;
QY 29 REGSEDLDALEHMFQRLRFESTWKRPDTAEOFOELEKFOQAIIDSDREDPVSCAFV 88
Db 258 RGTAKDKNLTLNLCMGYTVICKNLGTGRGMLTIRDFAK-----HSHGDSATLVILS 313
QY 89 HREGFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPGETV-----143
Db 314 HGENVIIGVDIPISITHEIYDLNANAPRLANKPKIVFVQACRGERDNGFPVLDSVD 373
QY 144 -----GGDEIWMVKDSP-----QTIPTTALHVSIVVEGYIAYR 179
Db 374 GVPAFLRRGWN-----RDGFLNFGICVRPQVQVWRKKPQADILLAYATAQYVSWR 428
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B56084
;Species: Homo sapiens (man)
;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
;Accession: B56084
;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
;Title: Cloning and expression of four novel isoforms of human interleukin-1beta convert

;Reference number: A56084; MUID:95181414; PID:7876192
;Accession: B56084
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-311 <ALN>
;Cross-references: GB:U13698; NID:G717041; PIDN:AAC50108.1; PID:G717042
;Genetics:
;Gene: IL1BCE
;Keywords: alternative splicing

Query Match 18.2%; Score 226; DB 2; Length 311;
Best Local Similarity 29.5%; Pred. No. 3.9e-10;
Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

Y 15 SGAALAILCVTK-----AREGSEEDLDALHMFRLPSTMKRDPPTAEQFQEELEKFP 69
b 67 SRTLLALICNEEFDSIPRTGAEDVTGTMLLQNLGYSVDVKKNLTASDMTTELEAFA 126
Y 70 QAIDSRDPVSCAFVYLMAHG-REGFLKGEDGMV-----KLENLFEALNNKNCQALRAKP 124
b 127 HRPEHKTS--DSTFLVFMHSHGIREGICGKHSEQVPDILQLNAIFNMLNTKNCPSLKDKP 184
Y 125 KVIILQACRGEQDGPGETVGDDEIVVMVKDS-----POTIPTYTDAL---HV---- 168
b 185 KVIILQACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEEFDDAIKKAHIEKDF 234
Y 169 ---YSTVEGYIAYRHDKQSCFIOTLVDFVTKRKHILEL-----LTEVTRMAEAEVLVQ 220
b 235 IAFCSSTPDNVSNRHPTMGSVFIQRLIE-----HMQEVACSDVEEIFRKVRFSFEQ 287
Y 221 EGKARKTNPIQSTLRKRLYL 241
b 288 DGRAQMPTE-RVLTTRCFYL 307

RESULT 13
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;Species: Homo sapiens (man)
;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
;Accession: A56084
;Alnemrl, E.S.; Fernandes-Alnemrl, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
;Title: Cloning and expression of four novel isoforms of human interleukin-1beta converting enzyme
;Reference number: A56084; MUID:95181414; PID:7876192
;Accession: A56084
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-383 <ALN>
;Cross-references: GB:U13697; NID:G717039; PIDN:AAC50107.1; PID:G717040
;Genetics:
;Gene: IL1BCE
;Keywords: alternative splicing

Query Match 18.2%; Score 226; DB 2; Length 383;
Best Local Similarity 29.5%; Pred. No. 3.9e-10;
Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

Y 15 SGAALAILCVTK-----AREGSEEDLDALHMFRLPSTMKRDPPTAEQFQEELEKFP 69
b 139 SRTLLALICNEEFDSIPRTGAEDVTGTMLLQNLGYSVDVKKNLTASDMTTELEAFA 198
Y 70 QAIDSRDPVSCAFVYLMAHG-REGFLKGEDGMV-----KLENLFEALNNKNCQALRAKP 124
b 199 HRPEHKTS--DSTFLVFMHSHGIREGICGKHSEQVPDILQLNAIFNMLNTKNCPSLKDKP 256
Y 125 KVIILQACRGEQDGPGETVGDDEIVVMVKDS-----POTIPTYTDAL---HV---- 168
b 257 KVIILQACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEEFDDAIKKAHIEKDF 306
Y 169 ---YSTVEGYIAYRHDKQSCFIOTLVDFVTKRKHILEL-----LTEVTRMAEAEVLVQ 220
b 307 IAFCSSTPDNVSNRHPTMGSVFIQRLIE-----HMQEVACSDVEEIFRKVRFSFEQ 359

Y 221 EGKARKTNPIQSTLRKRLYL 241
b 360 DGRAQMPTE-RVLTTRCFYL 379

RESULT 14
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;Species: Homo sapiens (man)
;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
;Accession: A42677; S21734; S24164
;Cerretti, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valenine, M.B.; Shapiro, D.N.; M
Genomics 20, 468-473, 1994
;Title: Molecular characterization of the gene for human interleukin-1beta converting e
;Reference number: A54263; MUID:94307734; PMID:8034320
;Accession: A54263
;Status: preliminary; not compared with conceptual translation
;Molecule type: DNA
;Residues: 1-404 <CE2>
;Cross-references: GB:L27475
;Cerretti, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A
Science 256, 97-100, 1992
;Title: Molecular cloning of the interleukin-1beta converting enzyme.
;Reference number: A42677; MUID:92229430; PMID:1373520
;Accession: A42677
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-404 <CE2>
;Cross-references: GB:M87507; NID:9433598; PIDN:AAA66942.1; PID:gl86286
;Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M.
J. Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Linjuco, G.; Palyha, O.C.; Raju, S.M.; Rol
cci, M.J.
Nature 356, 768-774, 1992
;Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proce
;Reference number: S21734; MUID:92244338; PMID:1574116
;Accession: S21734
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-404 <THO>
;Cross-references: EMBL:X55019; NID:G33792; PIDN:CAA46153.1; PID:G33793
;Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.;
Arch. Biochem. Biophys. 296, 698-703, 1992
;Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves
;Reference number: S24164; MUID:92337439; PMID:1321594
;Accession: S24164
;Status: preliminary
;Molecule type: Protein
;Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>
;Genetics:
;Gene: GDB:IL1BC
;Cross-references: GDB:132368; OMIM:147678
;Map position: 11q23-11q23
;Keywords: cysteine proteinase; hydrolase

Query Match 18.2%; Score 226; DB 2; Length 404;
Best Local Similarity 29.5%; Pred. No. 4.2e-10;
Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

Y 15 SGAALAILCVTK-----AREGSEEDLDALHMFRLPSTMKRDPPTAEQFQEELEKFP 69
b 160 SRTLLALICNEEFDSIPRTGAEDVTGTMLLQNLGYSVDVKKNLTASDMTTELEAFA 219
Y 70 QAIDSRDPVSCAFVYLMAHG-REGFLKGEDGMV-----KLENLFEALNNKNCQALRAKP 124
b 220 HRPEHKTS--DSTFLVFMHSHGIREGICGKHSEQVPDILQLNAIFNMLNTKNCPSLKDKP 277
Y 125 KVIILQACRGEQDGPGETVGDDEIVVMVKDS-----POTIPTYTDAL---HV---- 168
b 278 KVIILQACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEEFDDAIKKAHIEKDF 327
Y 169 ---YSTVEGYIAYRHDKQSCFIOTLVDFVTKRKHILEL-----LTEVTRMAEAEVLVQ 220

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Query Match      18.2%; Score 225; DB 2; Length 418;
Best Local Similarity 26.8%; Pred. No. 5.2e-10;
Matches 68; Conservative 53; Mismatches 85; Indels 48; Gaps 10;

19 LALILCVTK-----AREGSEEDLDALEHMFRLQRFESTKMDPTAEQFQEELEKFOQAID 73
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
178 LALII CNTRFDHLPANGAHYDIVGMKRLLOGLGTVTVDEKNTARDMESVLRAFAARPE 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

74 SRDPVSCAFVVLMAHG-REGFL-----KGEDGMVKLENLFEALNNKNCOLRAKPKVYI 128
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

238 HKAS--DSTFLVMHSHGILEGICGTAHKKKKDPVLLYDTYIQTFFNRNCLSLKKPKVII 295
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

129 IQACRGEQRPGETVGDEIVMWIKDSPOTIPTYT-----DALHYV 169
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

296 VQACRGEKH-GE-----LWVRDSPASLAVISSQSENLEADSVCKIHEEDXFIAC 345
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

170 STVEGYIAVEHDKGSCFIQTLVDVPTKK--GHILELLTETVTRMAEALVQEGKARKT 227
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

346 SSTPHNWSMDRTRGSIPTILITCQKYSCCCHLMETP---RKVQKSFVEVPQAKQMP 401
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

228 NPEIQSTLRKRLYL 241
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402 TIE-RATLTRDFYL 414
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Search completed: March 19, 2004, 11:24:53
Job time : 15.498 secs

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DM protein - protein search, using sw model

Run on: March 19, 2004, 11:24:16 ; Search time 34.2271 Seconds
(without alignments)

1830.924 Million cell updates/sec

Title: US-09-989-903-5

Perfect score: 1239

Sequence: 1 MSNPRSEEEKYDMSGAAAL.....KARKTNPEIQSTIRKELYIQ 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PCRT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1239	100.0	242	9	US-09-989-903-5
2	1239	100.0	242	14	US-10-068-564-5
3	1234	99.6	242	9	US-09-845-028-2
4	1234	99.6	242	10	US-09-851-873-105
5	1234	99.6	242	15	US-10-114-432-3
6	1234	99.6	242	15	US-10-114-432-15
7	1234	99.6	242	15	US-10-114-432-17
8	1234	99.6	242	15	US-10-114-432-18
9	1234	99.6	242	15	US-10-114-432-26
10	1234	99.6	242	15	US-10-114-432-27
11	1234	99.6	242	15	US-10-114-432-28
12	1234	99.6	242	15	US-10-114-432-30
13	1234	99.6	242	15	US-10-114-432-31
14	1234	99.6	242	15	US-10-114-432-67
15	1234	99.6	242	15	US-10-114-432-69

Sequence 71, Appl
Sequence 73, Appl
Sequence 13, Appl
Sequence 23, Appl
Sequence 37, Appl
Sequence 11, Appl
Sequence 22, Appl
Sequence 36, Appl
Sequence 9, Appl
Sequence 21, Appl
Sequence 66, Appl
Sequence 72, Appl
Sequence 24, Appl
Sequence 9, Appl
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Sequence 9, Appl
Sequence 29, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 34, Appl
Sequence 7, Appl
Sequence 5, Appl
Sequence 19, Appl
Sequence 64, Appl
Sequence 68, Appl
Sequence 35, Appl
Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-989-903-5

; Sequence 5, Application US/0989903

; Patent No. US20020146804A1

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; APPLICANT: Fernandez-Alnemri, Teresa

; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING

; TITLE OF INVENTION: AND METHODS OF USE

; FILE REFERENCE: 480140.434D1

; CURRENT APPLICATION NUMBER: US/09/989,903

; CURRENT FILING DATE: 2002-04-11

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 242

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-989-903-5

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Best Local Similarity 100.0%; Pred. No. 1.3e-113;

Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	FOELEKFPQQAIDREDPVSCAFVLMHAGREGFLKGEDGEMVKLENLFEALNNKCOAL	120
DB	61	FOELEKFPQQAIDREDPVSCAFVLMHAGREGFLKGEDGEMVKLENLFEALNNKCOAL	120
QY	121	RAKPNVYIIQACRGQORDPGTGVGDEIVMVVKDSPTIPTYTDALHVVSTVGGYIAYRH	180
DB	121	RAKPNVYIIQACRGQORDPGTGVGDEIVMVVKDSPTIPTYTDALHVVSTVGGYIAYRH	180
QY	181	DQKSGCFITLVDVFTKRGHILELLTEVTRMAEAEVQEGKARKTNPEIQSTLRKLY	240

us-09-989-903-5.rapb

181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
241 LQ 242
241 LQ 242

RESULT 2

3-10-068-564-5
Sequence 5, Application US/10068564
Publication No. US20030040096A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C2
CURRENT APPLICATION NUMBER: US/10/068,564
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien

S-10-068-564-5

Query Match 100.0%; Score 1239; DB 14; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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61 FOEELKFOAIDSRDPSVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
61 FOEELKFOAIDSRDPSVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
121 RAKPKVYIIQACRGEQDRPGETVGGDEIVWVKDSPTIPTTVDALHVVSTVEGYIAYRH 180
121 RAKPKVYIIQACRGEQDRPGETVGGDEIVWVKDSPTIPTTVDALHVVSTVEGYIAYRH 180
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
241 LQ 242
241 LQ 242

RESULT 3

S-09-845-028-2
Sequence 2, Application US/09845028
Patent No. US20020081705A1
GENERAL INFORMATION:
APPLICANT: Mankovich, John
TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
FILE REFERENCE: BSI-111
CURRENT APPLICATION NUMBER: US/09/845,028
CURRENT FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/199,962
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
S-09-845-028-2
Query Match 99.6%; Score 1234; DB 9; Length 242;

Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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121 RAKPKVYIIQACRGEQDRPGETVGGDEIVWVKDSPTIPTTVDALHVVSTVEGYIAYRH 180
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181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
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241 LQ 242
241 LQ 242

RESULT 4

US-09-851-873-105
Sequence 105, Application US/09851873
Publication No. US20030165488A1
GENERAL INFORMATION:
APPLICANT: Kietzien, Rolf F
APPLICANT: Reardon, Ilene M
APPLICANT: Weiland, Katherine L
TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
FILE REFERENCE: 28341/00233
CURRENT APPLICATION NUMBER: US/09/851,873
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-873-105

Query Match 99.6%; Score 1234; DB 10; Length 242;
Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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1 MSNPRSLBEKDYDMSGAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
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181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
241 LQ 242
241 LQ 242

RESULT 5

US-10-114-432-3
Sequence 3, Application US/10114432
Publication No. US20040019915A1

GENERAL INFORMATION:			Query Match	99.6%;	Score 1234;	DB 15;	Length 242;
APPLICANT: Challita-Eid, Pia M.			Best Local Similarity	99.6%;	Pred. No. 3.9e-113;		
APPLICANT: Raitano, Arthur B.			Matches 241;	Conservative	0;	Mismatches 1;	Indels 0;
APPLICANT: Paris, Mary							Gaps 0;
APPLICANT: Hubert, Rene S.							
APPLICANT: Morrison, Robert K.							
APPLICANT: Ge, Wangmao							
APPLICANT: Jakobovits, Aya							
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN							
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND							
TITLE OF INVENTION: DETECTION OF CANCER							
FILE REFERENCE: 51158-20066.00							
CURRENT APPLICATION NUMBER: US/10/114,432							
CURRENT FILING DATE: 2002-04-01							
NUMBER OF SEQ ID NOS: 88							
SOFTWARE: FastSeq for Windows Version 4.0							
SEQ ID NO 3							
LENGTH: 242							
TYPE: PRT							
ORGANISM: Homo Sapiens							
US-10-114-432-3							
Query Match			99.6%;	Score 1234;	DB 15;	Length 242;	
Best Local Similarity			99.6%;	Pred. No. 3.9e-113;			
Matches 241;			Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
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181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEVLVQEGKARKTNPEIQSTLRKRLY 240							
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241 LQ 242							
241 LQ 242							
RESULT 7							
US-10-114-432-17							
Sequence 17, Application US/10114432							
Publication No. US20040019915A1							
GENERAL INFORMATION:							
APPLICANT: Challita-Eid, Pia M.							
APPLICANT: Raitano, Arthur B.							
APPLICANT: Paris, Mary							
APPLICANT: Hubert, Rene S.							
APPLICANT: Morrison, Robert K.							
APPLICANT: Ge, Wangmao							
APPLICANT: Jakobovits, Aya							
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN							
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND							
TITLE OF INVENTION: DETECTION OF CANCER							
FILE REFERENCE: 51158-20066.00							
CURRENT APPLICATION NUMBER: US/10/114,432							
CURRENT FILING DATE: 2002-04-01							
NUMBER OF SEQ ID NOS: 88							
SOFTWARE: FastSeq for Windows Version 4.0							
SEQ ID NO 17							
LENGTH: 242							
TYPE: PRT							
ORGANISM: Homo Sapiens							
US-10-114-432-17							
Query Match			99.6%;	Score 1234;	DB 15;	Length 242;	
Best Local Similarity			99.6%;	Pred. No. 3.9e-113;			
Matches 241;			Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60							
1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60							
61 FQEELEKFOQAIDSREDPVSCAFVLMHAGREGFLKGEDGEMVKLENLFEALNNKCOAL 120							
61 FQEELEKFOQAIDSREDPVSCAFVLMHAGREGFLKGEDGEMVKLENLFEALNNKCOAL 120							
121 RAKPKVYIIQACRGEQDPGETVGGDEIVMVVKDSQPTIPTYTDALHVTSTVEGYIAYRH 180							
121 RAKPKVYIIQACRGEQDPGETVGGDEIVMVVKDSQPTIPTYTDALHVTSTVEGYIAYRH 180							
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEVLVQEGKARKTNPEIQSTLRKRLY 240							
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEVLVQEGKARKTNPEIQSTLRKRLY 240							
241 LQ 242							
241 LQ 242							
RESULT 6							
US-10-114-432-15							
Sequence 15, Application US/10114432							
Publication No. US20040019915A1							
GENERAL INFORMATION:							
APPLICANT: Challita-Eid, Pia M.							
APPLICANT: Raitano, Arthur B.							
APPLICANT: Paris, Mary							
APPLICANT: Hubert, Rene S.							
APPLICANT: Morrison, Robert K.							
APPLICANT: Ge, Wangmao							
APPLICANT: Jakobovits, Aya							
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN							
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND							
TITLE OF INVENTION: DETECTION OF CANCER							
FILE REFERENCE: 51158-20066.00							
CURRENT APPLICATION NUMBER: US/10/114,432							
CURRENT FILING DATE: 2002-04-01							
NUMBER OF SEQ ID NOS: 88							
SOFTWARE: FastSeq for Windows Version 4.0							
SEQ ID NO 15							
LENGTH: 242							
TYPE: PRT							
ORGANISM: Homo Sapiens							
US-10-114-432-15							

241 LQ 242

RESULT 8

S-10-114-432-18

Sequence 18, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

S-10-114-432-18

Query Match 99.6%; Score 1234; DB 15; Length 242;

Best Local Similarity 99.6%; Pred. No. 3.9e-113;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 MSNPRSLSEEEKYDMSGAAALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60

b 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60

Y 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120

b 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120

Y 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180

b 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180

Y 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQSGKARKTNPEIQSTLRKRLY 240

b 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQSGKARKTNPEIQSTLRKRLY 240

Y 241 LQ 242

b 241 LQ 242

RESULT 9

S-10-114-432-26

Sequence 26, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 26

; LENGTH: 242

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-114-432-26

Query Match 99.6%; Score 1234; DB 15; Length 242;

Best Local Similarity 99.6%; Pred. No. 3.9e-113;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGAAALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60

Db 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60

QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120

Db 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120

QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180

Db 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180

QY 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQSGKARKTNPEIQSTLRKRLY 240

Db 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQSGKARKTNPEIQSTLRKRLY 240

QY 241 LQ 242

Db 241 LQ 242

RESULT 10

US-10-114-432-27

; Sequence 27, Application US/10114432

; Publication No. US20040019915A1

; GENERAL INFORMATION:

; APPLICANT: Challita-Eid, Pia M.

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Paris, Mary

; APPLICANT: Hubert, Rene S.

; APPLICANT: Morrison, Robert K.

; APPLICANT: Ge, Wangmao

; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

; TITLE OF INVENTION: DETECTION OF CANCER

; FILE REFERENCE: 51158-20066.00

; CURRENT APPLICATION NUMBER: US/10/114,432

; CURRENT FILING DATE: 2002-04-01

; NUMBER OF SEQ ID NOS: 88

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 27

; LENGTH: 242

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-114-432-27

Query Match 99.6%; Score 1234; DB 15; Length 242;

Best Local Similarity 99.6%; Pred. No. 3.9e-113;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGAAALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60

Db 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60

QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120

Db 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120

QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180

Db 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180

181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKELY 240
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKELY 240
241 LQ 242
241 LQ 242

RESULT 11

US-10-114-432-28
Sequence 28, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-28

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 MSNPRSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
1 MSNPRSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
121 RAKPKVYIIQACRGEQDPGETVGGDEIVMVVKDPSQTIPTTIDALHVVSTVEGYIAYRH 180
121 RAKPKVYIIQACRGEQDPGETVGGDEIVMVVKDPSQTIPTTIDALHVVSTVEGYIAYRH 180
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKELY 240
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKELY 240
241 LQ 242
241 LQ 242

RESULT 12

US-10-114-432-30
Sequence 30, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-30

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 MSNPRSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
1 MSNPRSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
121 RAKPKVYIIQACRGEQDPGETVGGDEIVMVVKDPSQTIPTTIDALHVVSTVEGYIAYRH 180
121 RAKPKVYIIQACRGEQDPGETVGGDEIVMVVKDPSQTIPTTIDALHVVSTVEGYIAYRH 180
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKELY 240
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKELY 240
241 LQ 242
241 LQ 242

RESULT 13

US-10-114-432-31
Sequence 31, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-31

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 MSNPRSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
1 MSNPRSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60

61 FQEELEKFOQAIDSREDPVSCAFVLMHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
61 FQEELEKFOQAIDSREDPVSCAFVLMHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLY 240
181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLY 240
241 LQ 242
241 LQ 242

RESULT 14
S-10-114-432-67
Sequence 67, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213PIF11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114.432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
S-10-114-432-67

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
y 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRPSTWKRDPPTAEQ 60
b 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRPSTWKRDPPTAEQ 60
y 61 FQEELEKFOQAIDSREDPVSCAFVLMHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
b 61 FQEELEKFOQAIDSREDPVSCAFVLMHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
y 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
b 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
y 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLY 240
b 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLY 240
y 241 LQ 242
b 241 LQ 242

RESULT 15
S-10-114-432-69
Sequence 69, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213PIF11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114.432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 69
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-69

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRPSTWKRDPPTAEQ 60
DB 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRPSTWKRDPPTAEQ 60
QY 61 FQEELEKFOQAIDSREDPVSCAFVLMHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
DB 61 FQEELEKFOQAIDSREDPVSCAFVLMHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
QY 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLY 240
DB 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

Search completed: March 19, 2004, 11:33:36
Job time : 34.2271 secs

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M protein - protein search, using sw model

un on: March 19, 2004, 11:20:21 ; Search time 15.9084 Seconds
(without alignments)
785.341 Million cell updates/sec

title: US-09-989-903-5
effect score: 1239
equences: 1 MSNPRSLBEEKYDMSGALA.....KARKTNPEIQSLKRLYLQ 242

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Gapop 10.0 , Gapext 0.5

searched: 389414 seqs, 51625971 residues

otal number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/5A-COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCITUS-COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1239	100.0	242	4	US-09-187-789-5
2	1065	86.0	214	4	US-09-187-789-9
3	934.5	75.4	260	4	US-09-187-789-2
4	934.5	75.4	260	4	US-09-139-600-2
5	890	71.8	230	4	US-09-187-789-7
6	293	23.6	74	4	US-09-187-789-63
7	293	23.6	74	4	US-09-139-600-58
8	289	23.3	421	4	US-08-983-502-10
9	289	23.3	421	4	US-09-516-747-10
10	289	23.3	421	5	PCT-US96-10521-10
11	289	23.3	435	3	US-08-258-287B-53
12	289	23.3	435	3	US-08-368-704C-51
13	289	23.3	435	4	US-09-561-756-9
14	289	23.3	435	4	US-09-227-721-9
15	289	23.3	435	4	US-08-816-075-2
16	289	23.3	435	4	US-08-724-378D-9
17	289	23.3	435	4	US-09-954-697-9
18	289	23.3	435	5	PCT-US94-07127A-4
19	289	23.3	441	3	US-08-258-287B-44
20	289	23.3	441	3	US-08-368-704C-43
21	279	22.5	435	4	US-09-231-289-10
22	278.5	22.5	277	2	US-08-890-542A-2
23	273.5	22.1	277	3	US-08-591-605-2
24	273.5	22.1	277	3	US-08-964-308-6
25	273.5	22.1	277	3	US-08-462-969B-4
26	273.5	22.1	277	3	US-08-964-313-6
27	273.5	22.1	277	4	US-09-089-138-6

28	273.5	22.1	277	4	US-09-124-934A-4	Sequence 4, Appli
29	273.5	22.1	277	4	US-08-334-251D-4	Sequence 4, Appli
30	272.5	22.0	277	4	US-09-561-756-12	Sequence 12, Appli
31	272.5	22.0	277	4	US-09-227-721-12	Sequence 12, Appli
32	272.5	22.0	277	4	US-08-983-502-30	Sequence 30, Appli
33	272.5	22.0	277	4	US-08-724-378D-5	Sequence 5, Appli
34	272.5	22.0	277	4	US-09-516-747-30	Sequence 30, Appli
35	272.5	22.0	277	4	US-09-954-697-12	Sequence 12, Appli
36	272.5	22.0	277	5	PCT-US96-10521-30	Sequence 30, Appli
37	270.5	21.8	277	4	US-09-291-289-11	Sequence 11, Appli
38	263.5	21.3	277	3	US-08-964-308-10	Sequence 10, Appli
39	263.5	21.3	277	3	US-08-964-313-10	Sequence 10, Appli
40	263.5	21.3	277	4	US-09-089-138-10	Sequence 10, Appli
41	257	20.7	503	3	US-08-258-287B-36	Sequence 36, Appli
42	257	20.7	503	3	US-08-368-704C-36	Sequence 36, Appli
43	256	20.7	303	4	US-09-561-756-24	Sequence 24, Appli
44	256	20.7	303	4	US-09-227-721-24	Sequence 24, Appli
45	256	20.7	303	4	US-08-556-627A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-5

Query Match	100.0%	Score 1239;	DB 4;	Length 242;
Best Local Similarity	100.0%	Pred. No. 3.2e-122;		
Matches 242;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MSNPRSLBEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLRFEFTWKRPDPTAEQ	60	
Db	1	MSNPRSLBEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLRFEFTWKRPDPTAEQ	60	
Qy	61	FOBELEKFOQAIDSRDPPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKCOAL	120	
Db	61	FOBELEKFOQAIDSRDPPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKCOAL	120	
Qy	121	RAKPKYIIQACRGEDRDETVGGDEIVMWKDSPOIPIYTDALHYSTVEGVIAVRH	180	
Db	121	RAKPKYIIQACRGEDRDETVGGDEIVMWKDSPOIPIYTDALHYSTVEGVIAVRH	180	
Qy	181	DQKSGCFIQLVDVFTKRGHILELLTVTRRMAELVQEGKARKTNPEIQSTLRKELY	240	
Db	181	DQKSGCFIQLVDVFTKRGHILELLTVTRRMAELVQEGKARKTNPEIQSTLRKELY	240	
Qy	241	LQ 242		
Db	241	LQ 242		

RESULT 2

US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
S-09-187-789-9

Query Match 86.0%; Score 934.5; DB 4; Length 214;
Best Local Similarity 88.0%; Pred. No. 5.3e-104;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
Y 1 MSNPRSLSEBKDYMSGAALALILCVTKAREGSEEDLDALHMFRLRPFSTMKRDPTEAQ 60
b 1 MSNPRSLSEBKDYMSGARLALTLCVTKAREGSEVDMEALRMFRYLKFKSTMKRDPTEAQ 34
Y 61 FQELEKFOAIDSREDPVSACFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
b 35 --BELEKFOAIDSREDPVSACFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 92
Y 121 RAKPKVYIIQACRGEQORDPG-----ETVGGDEIVMVVKDSQPTIPTYTDALHY 180
b 93 RAKPKVYIIQACRGEQORDPG-----ETVGGDEIVMVVKDSQPTIPTYTDALHY 152
Y 181 DQKSGCFIOTLDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
b 153 DQKSGCFIOTLDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 212
Y 241 LQ 242
b 213 LQ 214

RESULT 3
S-09-187-789-2
Sequence 2, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
S-09-187-789-2

Query Match 75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 3.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
Y 1 MSNPRSLSEBKDYMSGAALALILCVTKAREGSEEDLDALHMFRLRPFSTMKRDPTEAQ 60
b 8 MSDPQLQEBRYDMSGARLALTLCVTKAREGSEVDMEALRMFRYLKFKSTMKRDPTEAQ 67
Y 61 FQELEKFOAIDSREDPVSACFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
b 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 127
Y 121 RAKPKVYIIQACRGEQORDPG-----ETVGGDEIVMVVKDSQPTIPTYTDALHY 168

Db 128 RGKPKVYIIQACRGEHDPGEELRGNBELGGDELVAVLKNPQSIPTIPTYDTLHI 186
QY 169 YSTVEGYIAYRHDKGSCFIOTLDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTN 228
Db 187 YSTVEGYLSYRHDEKSGFIOTLDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTN 246
QY 229 PEIQSTLRKRLY 242
Db 247 PEVQSTLRKRLY 260

RESULT 4
US-09-139-600-2
Sequence 2, Application US/09139600
Patent No. 6432628
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
US-09-139-600-2

Query Match 75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 3.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
QY 1 MSNPRSLSEBKDYMSGAALALILCVTKAREGSEEDLDALHMFRLRPFSTMKRDPTEAQ 60
Db 8 MSDPQLQEBRYDMSGARLALTLCVTKAREGSEVDMEALRMFRYLKFKSTMKRDPTEAQ 67
QY 61 FQELEKFOAIDSREDPVSACFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
Db 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 127
QY 121 RAKPKVYIIQACRGEQORDPG-----ETVGGDEIVMVVKDSQPTIPTYTDALHY 168
Db 128 RGKPKVYIIQACRGEHDPGEELRGNBELGGDELVAVLKNPQSIPTIPTYDTLHI 186
QY 169 YSTVEGYIAYRHDKGSCFIOTLDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTN 228
Db 187 YSTVEGYLSYRHDEKSGFIOTLDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTN 246
QY 229 PEIQSTLRKRLY 242
Db 247 PEVQSTLRKRLY 260

RESULT 5
US-09-187-789-7
Sequence 7, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 230

TYPE: PRT

ORGANISM: Homo sapien

S-09-187-789-7

Query Match 71.8%; Score 890; DB 4; Length 230;

Best Local Similarity 99.4%; Pred. No. 1.5e-85; Indels 0; Gaps 0;

Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 MSNPRLEEEKYDMSGAALALILCVTKAREGSEEDLDALHMFRLRPFSTWKRDPPTAEQ 60

b 1 MSNPRLEEEKYDMSGAALALILCVTKAREGSEEDLDALHMFRLRPFSTWKRDPPTAEQ 60

y 61 FQEELEKFOAIDSRDPVSCAFVVLMAHGREGLKGGEGWVKLENFEALNNKCOAL 120

b 61 FQEELEKFOAIDSRDPVSCAFVVLMAHGREGLKGGEGWVKLENFEALNNKCOAL 120

y 121 RAKPKVYIIQACRGEQRDPGETVGGDEIVWIKDSPQIPTYTDALHYSTVEG 174

b 121 RAKPKVYIIQACRGEQRDPGETVGGDEIVWIKDSPQIPTYTDALHYSTVEG 174

RESULT 6

S-09-187-789-63

Sequence 63, Application US/09187789

Patent No. 6340740

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING

FILE REFERENCE: 480140.434C1

CURRENT APPLICATION NUMBER: US/09/187,789

CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 63

LENGTH: 74

TYPE: PRT

ORGANISM: Mus musculus

S-09-187-789-63

Query Match 23.6%; Score 293; DB 4; Length 74;

Best Local Similarity 77.8%; Pred. No. 1.6e-23; Indels 0; Gaps 0;

Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

y 28 AREGSEEDLDALHMFRLRPFSTWKRDPPTAEQFQEELEKFOAIDSRDPVSCAFVVL 87

b 1 AREGSEVDMEALRFRYLFKFEFTWKRDPPTAQFLEELDEFQOTIDNWEPEVSCAFVVL 60

y 88 AHGREGFLKGED 99

b 61 AHGREGLLKGED 72

RESULT 7

S-09-139-600-58

Sequence 58, Application US/09139600

Patent No. 6432628

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING

FILE REFERENCE: 480140.434

CURRENT APPLICATION NUMBER: US/09/139,600

CURRENT FILING DATE: 1998-08-25

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 58

LENGTH: 74

TYPE: PRT

ORGANISM: Mus musculus

S-09-139-600-58

Query Match 23.6%; Score 293; DB 4; Length 74;

Best Local Similarity 77.8%; Pred. No. 1.6e-23; Indels 0; Gaps 0;

Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 AREGSEEDLDALHMFRLRPFSTWKRDPPTAEQFQEELEKFOAIDSRDPVSCAFVVL 87

Db 1 AREGSEVDMEALRFRYLFKFEFTWKRDPPTAQFLEELDEFQOTIDNWEPEVSCAFVVL 60

QY 88 AHGREGFLKGED 99

Db 61 AHGREGLLKGED 72

RESULT 8

US-08-983-502-10

; Sequence 10, Application US/08983502

; Patent No. 6399327

; GENERAL INFORMATION:

; APPLICANT: David WALLACH

; APPLICANT: Mark P. BOLDIN

; APPLICANT: Tanya M. GONCHAROV

; APPLICANT: Yuri V. GOLTSEV

; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF PAS RECEPTORS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street N.W., Ste. 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/983,502

; FILING DATE: 16-JAN-1998

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/10521

; FILING DATE: 14-JUN-1996

; APPLICATION DATA:

; APPLICATION NUMBER: IL 114,615

; FILING DATE: 16-JUL-1995

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: IL 114,986

; FILING DATE: 17-AUG-1995

; APPLICATION DATA:

; APPLICATION NUMBER: IL 115,319

; FILING DATE: 14-SEP-1995

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: IL 116,588

; FILING DATE: 27-DEC-1995

; APPLICATION DATA:

; APPLICATION NUMBER: IL 117,932

; FILING DATE: 16-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Browdy, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: WALLACH=19

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 628-5197

; TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 421 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

3-08-983-502-10

Query Match 23.3%; Score 289; DB 4; Length 421;
Best Local Similarity 31.1%; Pred. No. 5.2e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
US-09-516-747-10

29 REGSEEDLDALEHMFQRLPSTWKRDPDTAQPQOELEKFKQAIDSREDPVSCAFVVLMA 88
188 RSGGDVHSTLVTFLKLGVDVHVLCDQTAQEMQKLNFAQ-LPAHRVTDSC-IVALLS 245
89 HGRGFLKGDGEMVKLENLFEALNNKNCALRAKPKVYIIQACRGEQDPG----- 140
246 HGVEGAIYGVGDKLLQLEVFQFDNANCPSLQNKPMFFIACRGEDETDRGVDDQDGN 305
141 -----ETVGGDIWVVIKDSPTIPTYTDALHVVSTVEGYIAYRHDKGSCFTQTLV 192
306 HAGSPGCEESDAGKE-----KLPKRLPTRSDMICGYACLKGTAAAMNTRKGSWYIEALA 360
193 DVFTKR--KGHILELLTVTRMAEALVQSGKARKTN-----PEIQSTLRKRLYL 241
361 QVFSERACDMHVADMLVKVNALIKD-----REGYAPGTFEHRCKEMSEYCSILCRHLYL 414

RESULT 9

S-09-516-747-10
Sequence 10, Application US/09516747
Patent No. 6586571

GENERAL INFORMATION:

APPLICANT: David WALLACH
Mark P. BOLDIN
Tanya M. GONCHAROV
Yury V. GOLTSEV

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,747
FILING DATE: 01-Mar-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/983,502
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Broadway, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-516-747-10

Query Match 23.3%; Score 289; DB 4; Length 421;
Best Local Similarity 31.1%; Pred. No. 5.2e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
US-09-516-747-10

QY 29 REGSEEDLDALEHMFQRLPSTWKRDPDTAQPQOELEKFKQAIDSREDPVSCAFVVLMA 88
DB 188 RSGGDVHSTLVTFLKLGVDVHVLCDQTAQEMQKLNFAQ-LPAHRVTDSC-IVALLS 245
QY 89 HGRGFLKGDGEMVKLENLFEALNNKNCALRAKPKVYIIQACRGEQDPG----- 140
DB 246 HGVEGAIYGVGDKLLQLEVFQFDNANCPSLQNKPMFFIACRGEDETDRGVDDQDGN 305
QY 141 -----ETVGGDIWVVIKDSPTIPTYTDALHVVSTVEGYIAYRHDKGSCFTQTLV 192
DB 306 HAGSPGCEESDAGKE-----KLPKRLPTRSDMICGYACLKGTAAAMNTRKGSWYIEALA 360
QY 193 DVFTKR--KGHILELLTVTRMAEALVQSGKARKTN-----PEIQSTLRKRLYL 241
DB 361 QVFSERACDMHVADMLVKVNALIKD-----REGYAPGTFEHRCKEMSEYCSILCRHLYL 414

RESULT 10

PCT-US96-10521-10
Sequence 10, Application PC/TUS9610521
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
NUMBER OF SEQUENCES: 34

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10521-10

Query Match 23.3%; Score 289; DB 5; Length 421;
Best Local Similarity 31.1%; Pred. No. 5.2e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

Y 29 REGSEEDLDALHMFQRLPSTFKRDPDTAEQFOBELEKFOQADSDREDPVSCAFVILMA 88
b 188 RSGGDVDHSTLVTFLKGLGYDVHVLCDQTAQEMQEKLNQFAQ-LPAHRVTDSC-IVALLS 245
Y 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDQPG-----140
b 246 HGVEGAIYGVGKLLQLEVFQFDNANCPSLQNKPKMFFIACRGGDETDGVDQDQGN 305
Y 141 -----ETVGGDEIWMVKIDSPQTIPTDHALHYSTVEGYIAYRHDKGSCFIQTLV 192
b 306 HAGSPGCEESDAGKE-----KLPKMRLPTRSDMICGYACLKGTAAAMRNTKRGSWYIEALA 360
Y 193 DVFTKR--KGHILELLETVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
b 361 QVFSERACDMHVDMLVKVNALIKD-----REGYAPGTFFHRCCKEMSEYCVSTLCRHLYL 414

RESULT 11
US-08-258-287B-53
Sequence 53, Application US/08258287B
Patent No. 6083735
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,287B
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3920001
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-258-287B-53

Query Match 23.3%; Score 289; DB 3; Length 435;
Best Local Similarity 31.1%; Pred. No. 5.4e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
Y 29 REGSEEDLDALHMFQRLPSTFKRDPDTAEQFOBELEKFOQADSDREDPVSCAFVILMA 88
b 202 RSGGDVDHSTLVTFLKGLGYDVHVLCDQTAQEMQEKLNQFAQ-LPAHRVTDSC-IVALLS 259
Y 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDQPG-----140
b 260 HGVEGAIYGVGKLLQLEVFQFDNANCPSLQNKPKMFFIACRGGDETDGVDQDQGN 319

QY 141 -----ETVGGDEIWMVKIDSPQTIPTDHALHYSTVEGYIAYRHDKGSCFIQTLV 192
DB 320 HAGSPGCEESDAGKE-----KLPKMRLPTRSDMICGYACLKGTAAAMRNTKRGSWYIEALA 374
QY 193 DVFTKR--KGHILELLETVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
DB 375 QVFSERACDMHVDMLVKVNALIKD-----REGYAPGTFFHRCCKEMSEYCVSTLCRHLYL 428
RESULT 12
US-08-368-704C-51
Sequence 51, Application US/08368704C
Patent No. 6087160
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,704C
FILING DATE: 4-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3920002
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-368-704C-51

Query Match 23.3%; Score 289; DB 3; Length 435;
Best Local Similarity 31.1%; Pred. No. 5.4e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
QY 29 REGSEEDLDALHMFQRLPSTFKRDPDTAEQFOBELEKFOQADSDREDPVSCAFVILMA 88
DB 202 RSGGDVDHSTLVTFLKGLGYDVHVLCDQTAQEMQEKLNQFAQ-LPAHRVTDSC-IVALLS 259
QY 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDQPG-----140
DB 260 HGVEGAIYGVGKLLQLEVFQFDNANCPSLQNKPKMFFIACRGGDETDGVDQDQGN 319
QY 141 -----ETVGGDEIWMVKIDSPQTIPTDHALHYSTVEGYIAYRHDKGSCFIQTLV 192
DB 320 HAGSPGCEESDAGKE-----KLPKMRLPTRSDMICGYACLKGTAAAMRNTKRGSWYIEALA 374

y 193 DVFTKR--KGHILELLTEVTRRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
b 375 QVESBRACDMHVADMLVKYNALIKD-----REGYAPGTBFHRCCKEMSEYCYSTLCRHLYL 428

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ob time : 16.9084 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: March 19, 2004, 11:08:15 ; Search time 49.1713 Seconds
(without alignments)
1390.577 Million cell updates/sec

title: US-09-989-903-5
perfect score: 1239
sequence: 1 MSNPSLEBEKYDMSGALLA.....KARKTNPIQSTLRKLYIQ 242

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 1586107 seqs, 282547505 residues

total number of hits satisfying chosen parameters: 1586107

minimum DB seq length: 0
maximum DB seq length: 2000000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB	ID	Description
1	1234	99.6	242	3	AAV93214	Aay93214 Amino aci
2	1234	99.6	242	5	AAV97980	Aag77980 Full-leng
3	1189	96.0	242	5	AAV97984	Aag77984 Full-leng
4	1166	94.1	229	3	AAV68865	Aay68865 Amino aci
5	1065	86.0	214	3	AAV93216	Aay93216 Amino aci
6	934.5	75.4	257	3	AAV68864	Aay68864 Amino aci
7	934.5	75.4	281	2	AAV93592	Aaw93592 Mouse cas
8	934.5	75.4	281	3	AAV93213	Aay93213 Amino aci
9	890	71.8	230	3	AAV93215	Aay93215 Amino aci
10	472.5	38.1	234	3	AAU72882	Aau72882 Human asp
11	472.5	38.1	398	5	ABG76499	Abg76499 DNA encod
12	295	23.8	452	5	ABB10110	Abb10110 Mouse cas
13	293	23.6	452	7	ADB79812	Adb79812 Rat caspa
14	293	23.6	452	7	ADE63000	Ad63000 Rat Prote
15	289	23.3	435	2	AAV66771	Aar66771 Human int
16	289	23.3	435	2	AAV98462	Aar98462 Human int
17	289	23.3	435	2	AAV90703	Aar90703 Interleuk
18	289	23.3	435	2	AAW26274	Aaw26274 Cell deat
19	289	23.3	435	2	AAV21716	Aay21716 Amino aci
20	289	23.3	435	3	AAV14257	Aab14257 Human ich
21	289	23.3	435	4	AAE00599	Aae00599 Human cas
22	289	23.3	435	5	ABV78321	Abv78321 Amino aci
23	289	23.3	435	5	ABJ01217	Abj01217 Human cas
24	289	23.3	435	7	ADE63002	Ad63002 Human pro
25	289	23.3	441	2	AAV66768	Aar66768 Human int

AAV14253 Human ich
AAB59579 Human cas
ADE63080 Rat Prote
AAW47089 Rat inter
AAE00610 Chimeric
AAB14262 Mutant hu
AAG78712 Pig caspa
AAB26763 Human cas
AAW00372 Apopain C
AAR95831 Human int
AAW00677 Pro-Yama.
AAW41688 Amino aci
AAU05395 Mouse cas
AAO19867 Bacteriop
Add25641 Binding d
AAm25766 Human pro
AAW16600 Apopain C
AAY21171 Amino aci
AAU05394 Human cas
AAE00600 Human cas

ALIGNMENTS

RESULT 1
AAV93214
ID AAY93214 standard; protein; 242 AA.
XX AC AAY93214;
XX AC AAY93214;
DT 04-SEP-2000 (first entry)
XX DB Amino acid sequence of a human caspase-14.
XX KW Caspase-14; cell death specific protease; apoptosis stimulator;
KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX OS Homo sapiens.
XX FH Key
XX FT Region 1..146 Location/Qualifiers
FT /note= "large subunit"
FT Active-site 130..134
FT Cleavage-site 146..147
FT Region 146..242
FT /note= "small subunit"
XX WO200028047-A1.
XX 18-MAY-2000.
XX 29-OCT-1999; 99WO-US025523.
XX 06-NOV-1998; 98US-00187789.
XX (UVJE-) UNIV JEFFERSON THOMAS.
XX PI Alnemri BS, Fernandez-Alnemri T;
XX WPI; 2000-376558/32.
XX N-PSDB; AAA15164.
XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
XX Claim 13; Fig 7; 78pp; English.

The present sequence represents a human caspase-14 polypeptide. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of

C apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
C diseases and ischemic injury are treated by administering anti-caspase-14
C antibodies. The antibody is useful for determining the presence or the
C level of caspase-14 in tissue sample and also for the isolation of
C caspase-14 with apoptotic activity or in screening assay to identify an
C agent that inhibits heterodimer or heterotetramer formation and
C therefore, apoptosis
X
Q Sequence 242 AA;
Query Match 99.6%; Score 1234; DB 3; Length 242;
Best Local Similarity 99.6%; Pred. No. 1.5e-120;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1 MSNPRSEEEKYDMSGAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPDAEQ 60
b 1 MSNPRSEEEKYDMSGAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPDAEQ 60
Y 61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQCAL 120
b 61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQCAL 120
Y 121 RAKPKVYIIQACRGEQDPGETVGGDEIWMVVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
b 121 RAKPKVYIIQACRGEQDPGETVGGDEIWMVVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
Y 181 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
b 181 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
Y 241 LQ 242
b 241 LQ 242

RESULT 2
AG77980
D AAG77980 standard; protein; 242 AA.
X AAG77980;
X
T 05-APR-2002 (first entry)
X Full-length human caspase-14.
E Human; caspase-14; anti-apoptotic; apoptosis.
W Homo sapiens.
S WO200181595-A2.
N 01-NOV-2001.
X 27-APR-2001; 2001WO-US013831.
X 27-APR-2000; 2000US-0199962P.
R (KNOL) KNOLL GMBH.
A Mankovich JA;
I WPI; 2002-041410/05.
R N-PSDB; AAK98248.
X Novel isolated human caspase-14 proteins and nucleic acid sequences,
T useful for identifying modulators of caspase-14 protein that are useful
T for modulating apoptosis.
S Claim 20; Fig 1; 58pp; English.
X
X The sequence represents the novel full-length human caspase-14 protein,
C referred to as "Caspase-14 NW" in the specification. The invention
C relates to a novel isolated human caspase-14 protein comprising an amino

CC acid sequence with MSNPRSEEE, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein
XX
SQ Sequence 242 AA;

Query Match 99.6%; Score 1234; DB 5; Length 242;
Best Local Similarity 99.6%; Pred. No. 1.5e-120;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSNPRSEEEKYDMSGAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPDAEQ 60
Db 1 MSNPRSEEEKYDMSGAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPDAEQ 60
QY 61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQCAL 120
Db 61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQCAL 120
QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIWMVVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
Db 121 RAKPKVYIIQACRGEQDPGETVGGDEIWMVVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
QY 181 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
Db 181 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
QY 241 LQ 242
Db 241 LQ 242

RESULT 3
AAG77984
ID AAG77984 standard; protein; 242 AA.
XX AAG77984;
XX
DT 05-APR-2002 (first entry)
XX Full-length human caspase-14 old.
DE Human; caspase-14; anti-apoptotic; apoptosis.
KW Homo sapiens.
OS WO200181595-A2.
PN 01-NOV-2001.
XX 27-APR-2001; 2001WO-US013831.
XX 27-APR-2000; 2000US-0199962P.
XX (KNOL) KNOLL GMBH.
XX Mankovich JA;
XX WPI; 2002-041410/05.
XX Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.

Example; Fig 1; 58pp; English.

The sequence represents the full-length human caspase-14 protein, referred to as "Caspase-14 OLD" in the specification. The invention relates to a novel isolated human caspase-14 protein comprising an amino acid sequence with MSNPRSLRE, at its amino terminus. The caspase-14 of the invention has anti-apoptotic activity. Caspase-14 acts as a modulator of caspase-14 activity. The polypeptide is useful for identifying a compound which is a modulator of human caspase-14 activity, and is also useful for identifying a compound which modulates the interaction of caspase-14 with a target molecule. An antibody to caspase-14 is useful for isolating the protein by standard techniques, and for detecting caspase-14 to evaluate the abundance and expression pattern. The antibody is also useful for diagnostically monitoring protein levels in a tissue or sample. The polypeptide is useful as a tissue or sample for screening assays, and as a bait protein in a two-hybrid or three-hybrid assay to identify other proteins that interact with human caspase-14 protein.

Sequence 242 AA;

Query Match 96.0%; Score 1189; DB 5; Length 242;
Best Local Similarity 99.6%; Pred. No. 7.6e-116;
Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
10 EKYDMSGALALILCVTKAREGSBEDLDALHMPRLRFRFSTMKRDPRTAQFOBELEKFO 69
10 EKYDMSGALALILCVTKAREGSBEDLDALHMPRLRFRFSTMKRDPRTAQFOBELEKFO 69
70 QAIDREDPVS CAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYII 129
70 QAIDREDPVS CAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYII 129
130 QACRGDPGTGSGDEIVMWIKDSPOTIPTYTDALHVSSTVEGYIAYRHDKGSCFIQ 189
130 QACRGDPGTGSGDEIVMWIKDSPOTIPTYTDALHVSSTVEGYIAYRHDKGSCFIQ 189
190 TLVDVFTKKGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLYLQ 242
190 TLVDVFTKKGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLYLQ 242

RESULT 4
AY68865
D RAY68865 standard; protein; 229 AA.

AY68865;
15-MAY-2000 (first entry)
E Amino acid sequence of a human caspase-like polypeptide.
E Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
W keratinisation; wound healing.

S Homo sapiens.
X WO200004169-A1.
N 27-JAN-2000.
D 12-JUL-1999; 99WO-EP004939.
F 17-JUL-1998; 98EP-00202422.
X (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
A Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
I WPI; 2000-182433/16.
R N-PSDB; AAZ60684.

XX New murine and human caspase homologues useful for treating skin related disorders.

Claim 2; Page 53-54; 68pp; English.

The present sequence represents a human caspase-like polypeptide. The specification also describes a murine caspase-like polypeptide. Caspases are cysteinyl aspartate-specific proteinases which play a central role in apoptosis. The polypeptides of the invention are related to human and murine caspase-2 and human caspase-9, and possess all of the typical amino acids involved in catalysis, including the QACRG box, and contain no or only a very short prodomain. mRNA expression of the homologues of the invention is predominant in the skin. The caspase-like polypeptides are useful for treating human or animal diseases, such as skin diseases. They are also useful for screening for compounds that modulate its activity, i.e. agonists, antagonists, and inhibitors. The caspase-like polypeptides and polynucleotides are useful for modulating keratinisation, for diagnosing and treating inappropriate wound healing protein

Sequence 229 AA;

Query Match 94.1%; Score 1166; DB 3; Length 229;
Best Local Similarity 99.6%; Pred. No. 1.8e-113;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
14 MSGAALALILCVTKAREGSBEDLDALHMPRLRFRFSTMKRDPRTAQFOBELEKFOAID 73
1 MSGAALALILCVTKAREGSBEDLDALHMPRLRFRFSTMKRDPRTAQFOBELEKFOAID 60
74 SREDPVS CAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACR 133
61 SREDPVS CAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACR 120
134 GEORDPGTGSGDEIVMWIKDSPOTIPTYTDALHVSSTVEGYIAYRHDKGSCFIQTLVD 193
121 GEORDPGTGSGDEIVMWIKDSPOTIPTYTDALHVSSTVEGYIAYRHDKGSCFIQTLVD 180
194 VFTKKGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLYLQ 242
181 VFTKKGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLYLQ 229

RESULT 5
AY93216
ID AAY93216 standard; protein; 214 AA.
XX AC AAY93216;
XX 04-SEP-2000 (first entry)
DT Amino acid sequence of a human caspase-14 splice variant.
DE Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.
KW Homo sapiens.
OS Key Location/Qualifiers
FH Active-site 102..106
FT WO200028047-A1.
XX 18-MAY-2000.
XX 29-OCT-1999; 99WO-US025523.
PF 06-NOV-1998; 98US-00187789.
PR (UYJE-) UNIV JEFFERSON THOMAS.
XX Alnemri ES, Fernandez-Alnemri T;
XX

WPI; 2000-376558/32.
N-PSDB; AAA15166.
Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
Claim 42; Fig 9; 78pp; English.
The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence of the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an agent that inhibits heterodimer or heterotetramer formation and therefore, apoptosis
Sequence 214 AA;
Query Match 86.0%; Score 1065; DB 3; Length 214;
Best Local Similarity 88.0%; Pred. No. 6.2e-103;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
1 MSNPSLEEKYDMSGALALILCVTKAREGSEDLDALEHMFQLRFESTMKRDPTAEQ 60
1 MSNPSLEEKYDMSGALALILCVTKAREGSEDLDALEHMFQLRFESTMKRDPTAEQ 60
61 FOEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
35 --EELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 92
121 RAKPKVYIIQACRGQRDPGETVGDEIVMWIKDSPTIPTYTDLHVSTVSGYIAYRH 180
93 RAKPKVYIIQACRGQRDPGETVGDEIVMWIKDSPTIPTYTDLHVSTVSGYIAYRH 152
181 DQKSGCFIQTLDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPIQSTLRKRLY 240
153 DQKSGCFIQTLDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPIQSTLRKRLY 212
241 IQ 242
213 LQ 214
RESULT 6
AY68864
RAY68864 standard; protein; 257 AA.
RAY68864;
16-MAY-2000 (first entry)
Amino acid sequence of a murine caspase-like polypeptide.
Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease; keratinisation; wound healing.
Mus musculus.
WO200004169-A1.
27-JAN-2000.
12-JUL-1999; 99WO-BF004939.
17-JUL-1998; 98EP-00202422.
(VLA--) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

PI Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
XX WPI; 2000-182433/16.
DR N-PSDB; AAZ60683.
XX New murine and human caspase homologues useful for treating skin related disorders.
PT
XX
PS Claim 1; Page 51-52; 68pp; English.
XX The present sequence represents a murine caspase-like polypeptide. The specification also describes a human caspase-like polypeptide. Caspases are cysteinyl aspartate-specific proteinases which play a central role in apoptosis. The polypeptides of the invention are related to human and murine caspase-2 and human caspase-9, and possess all of the typical amino acids involved in catalysis, including the QACRG box, and contain no or only a very short prodomain. mRNA expression of the homologues of the invention is predominant in the skin. The caspase-like polypeptides are useful for treating human or animal diseases, such as skin diseases. They are also useful for screening for compounds that modulate its activity, i.e. agonists, antagonists, and inhibitors. The caspase-like polypeptides and polynucleotides are useful for modulating keratinisation, for diagnosing and treating inappropriate wound healing
XX Sequence 257 AA;
SQ
Query Match 75.4%; Score 934.5; DB 3; Length 257;
Best Local Similarity 70.9%; Pred. No. 3.8e-89;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
QY 1 MSNPSLEEKYDMSGALALILCVTKAREGSEDLDALEHMFQLRFESTMKRDPTAEQ 60
DB 5 MSDFQPIQEEYDMSGARLALTLCTVKAREGSEVDMEALRMFYLKFEETMKRDPTAQ 64
QY 61 FOEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 65 FLEELDFEQITDINWEEPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCAL 124
QY 121 RAKPKVYIIQACRGQRDPG-----BTVGDEIVMWIKDSPTIPTYTDLHV 168
DB 125 RGPVKVYIIQACRGHRDPGEELRGNEELGGDEELGGDE--VAVLKNPQSIPTYDTLHI 183
QY 169 YSTVEGYIAYRHDKGSCFIQTLDVFTKRGHILELLTEVTRMAEALVQEGKARKTN 228
DB 184 YSTVEGYIAYRHDKGSGFIQTLDVFTKRGHILELLTEVTRMAEALVQEGKARKTN 243
QY 229 PEIQTSLRKRLYLQ 242
DB 244 PEVQSTLRKRLYLQ 257
RESULT 7
AAW93592
ID AAW93592 standard; protein; 281 AA.
XX
AC AAW93592;
XX
DT 21-JUN-1999 (first entry)
XX
DE Mouse caspase-14 protein.
XX
KW Caspase-14; murine; protease; treatment; apoptotic-related disease; autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS; neurodegenerative disease; ischaemic injury; anti-idiotypic antibody; caspase-14 processing activity; epitope; competitor; modulator.
OS Mus sp.
FN WO9910504-A2.
XX
PD 04-MAR-1999.
XX
XX 26-AUG-1998; 98WO-US017715.

X R 26-AUG-1997; 97US-0056986P.
X A (IDUN-) IDUN PHARM INC.
X I Alnemri ES, Fernandes-Alnemri T;
X R WPI; 1999-204670/17.
X R N-PSDB; AAX23515.
X T Newly isolated polynucleotide encoding a caspase-14 polypeptide - useful
T for identifying (ant)agonists that are useful in the diagnosis and
T treatment of apoptosis-related diseases.
X X Claim 4; Fig 1; 59pp; English.
X C This invention describes a novel murine caspase-14 which has protease
C activity. The caspase-14 polypeptide is useful for identifying
C (ant)agonists of the polypeptide, where enzyme activity is measured with
C a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated
C caspase-14 is useful for identifying inhibitors or enhancers of caspase-
C 14 activity. The compounds identified by both methods form pharmaceutical
C compositions for treating apoptotic-related diseases, including
C autoimmune disease, cancer, acquired immunodeficiency syndrome (AIDS),
C neurodegenerative diseases and ischaemic injury. The anti-caspase-14
C antibody is useful for measuring the level of caspase-14 in a tissue
C sample. An antibody that binds to a caspase-14 polypeptide is useful for
C isolating the polypeptide, and an antibody that binds to the large or
C small subunit the polypeptide is useful for identifying samples with
C caspase-14 processing activity. An antibody that binds to caspase-14
C heterodimer or heterotetramer is useful for isolating caspase-14 with
C apoptotic activity or in a screening assay to identify (ant)agonists. The
C antibodies form kits for such purposes. The anti-caspase-14 antibody is
C also useful for preparing anti-idiotypic antibodies, which mimic a
C caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,
C the antibody is useful as a competitor of caspase-14 in reducing the
C level of caspase-14 activity, which reduces the level of apoptotic
C activity. Oligonucleotides made from the polynucleotides are useful as
C polymerase chain reaction (PCR) primers or probes to screen genomic or
C cDNA libraries for similar caspase-14 encoding polynucleotides, or for
C diagnosis of diseases associated with enhanced or inhibited apoptosis.
C The isolated caspase-14 gene permits methods of modulating apoptosis for
C the treatment of human diseases
X X Sequence 281 AA;
Query Match 75.4%; Score 934.5; DB 2; Length 281;
Best Local Similarity 70.9%; Pred. No. 4.3e-89;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
Y 1 MSNPRLEEEKYDMSGALALILCVTKAREGSEEDLDALHEHFRQLRPFESTMKRDPTAEQ 60
b 24 MSDPQLQEERYDMSGARLALTLCVTKAREGSEVDMEALRMFRYLKPFESTMKRDPTAAQ 83
Y 61 FOELEKFOAIDSDREDPVSCAFVLMHAGREGFLKGEDEGMVKLENLFEALNNKNCAL 120
b 84 FLEELDFEQTTDNWEEPVSCAFVLMHAGREGFLKGEDEKVRLEDLFEVLNNKNCAL 143
Y 121 RAKPKVYIIQACRGEQDPG-----ETVGGDEIVVMVKDSQPTIPTYTDALHV 168
b 144 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPNQSIPTYTDLHI 202
Y 169 YSTVEGVYIYRHQKSGCFQTQTVLVFTKRGHILELLTEVTRMAEELVQEGKARKTN 228
b 203 YSTVEGVLSYRHEKSGSGFIQTITDVFTHKKSILELLEITELMANTVEVQEGPRKN 262
Y 229 PETQSTLRKLYLQ 242
b 263 FEVQSTLRKLYLQ 276
RESULT 8
AY93213

ID AAY93213 standard; protein; 281 AA.
XX AAY93213;
XX 04-SEP-2000 (first entry)
XX Amino acid sequence of a murine caspase-14.
XX Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX Mus sp.
XX Key Location/Qualifiers
XX Region 1..156
XX /note="large subunit"
XX Active-site 134..138
XX Cleavage-site 156..157
XX Cleavage-site 162..163
XX Region 163..257
XX /note="small subunit"
XX WO200028047-A1.
XX 18-MAY-2000.
XX 29-OCT-1999; 99WO-US025523.
XX 06-NOV-1998; 98US-00187789.
XX (UYJB-) UNIV JEFFERSON THOMAS.
XX Alnemri ES, Fernandez-Alnemri T;
XX WPI; 2000-376858/32.
XX N-PSDB; AAL15163.
XX Novel nucleic acids encoding cell death specific protease termed caspase-
XX 14 useful for treating cancers by stimulating apoptosis.
XX Claim 52; Fig 1; 78pp; English.
XX The present sequence represents a murine caspase-14 polypeptide. The
XX polypeptide is a cell death specific protease, and is an apoptosis
XX stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
XX -14 antibodies are useful for treating or reducing the severity of
XX pathological conditions associated with increased or decreased levels of
XX apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
XX diseases and ischemic injury are treated by administering anti-caspase-14
XX antibodies. The antibody is useful for determining the presence or the
XX level of caspase-14 in tissue sample and also for the isolation of
XX caspase-14 with apoptotic activity or in screening assay to identify an
XX agent that inhibits heterodimer or heterotetramer formation and
XX therefore, apoptosis
XX Sequence 281 AA;
Query Match 75.4%; Score 934.5; DB 3; Length 281;
Best Local Similarity 70.9%; Pred. No. 4.3e-89;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
QY 1 MSNPRLEEEKYDMSGALALILCVTKAREGSEEDLDALHEHFRQLRPFESTMKRDPTAEQ 60
Db 24 MSDPQLQEERYDMSGARLALTLCVTKAREGSEVDMEALRMFRYLKPFESTMKRDPTAAQ 83
QY 61 FOELEKFOAIDSDREDPVSCAFVLMHAGREGFLKGEDEGMVKLENLFEALNNKNCAL 120
Db 84 FLEELDFEQTTDNWEEPVSCAFVLMHAGREGFLKGEDEKVRLEDLFEVLNNKNCAL 143
QY 121 RAKPKVYIIQACRGEQDPG-----ETVGGDEIVVMVKDSQPTIPTYTDALHV 168
Db 144 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPNQSIPTYTDLHI 202

169 YSTVEGYIAYRHDKGSCFIOTLVDFVFKRGHILELLTEVTRMAEALVQSGKARKTN 228
203 YSTVEGYLSYRDEKSGSFIOTLVDFVFKRGHILELLTEVTRMAEALVQSGKARKTN 262
229 PEIQSTLAKRLYLQ 242
263 PEVQSTLAKRLYLQ 276

RESULT 9
AY93215
J AAY93215 standard; protein; 230 AA.
K AAY93215;
L AAY93215;
I 04-SEP-2000 (first entry)
E Amino acid sequence of a human caspase-14 splice variant.
X Caspase-14; cell death specific protease; apoptosis stimulator;
W apoptosis; AIDS; neurodegenerative disease; ischemic injury.
S Homo sapiens.
H Key Location/Qualifiers
I Active-site 130..134
X WO2000028047-A1.
N 18-MAY-2000.
D 29-OCT-1999; 99WO-US025523.
F 06-NOV-1998; 98US-00187789.
R (UYJE-) UNIV JEFFERSON THOMAS.
A Alnemri ES, Fernandez-Alnemri T;
I WPI; 2000-376558/32.
R N-PSDB; AAA15165.
T Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
X Claim 41; Fig 8; 78pp; English.
S The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence or the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an agent that inhibits heterodimer or heterotetramer formation and therefore, apoptosis

Query Match 71.8%; Score 890; DB 3; Length 230;
Best Local Similarity 99.4%; Pred. NO. 1.5e-84;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 MSNPSLEEEKYDMSGAALILCVTKAREGSEEDLDALHMFRLRFEFTMKRDPTRAEQ 60
b 1 MSNPSLEEEKYDMSGAALILCVTKAREGSEEDLDALHMFRLRFEFTMKRDPTRAEQ 60
Y 61 FQBELEKFOAIDSRDPPVSCAFVLMVMAHGRGFLKGDGEMVKLENLFEALNNKCOAL 120
b 61 FQBELEKFOAIDSRDPPVSCAFVLMVMAHGRGFLKGDGEMVKLENLFEALNNKCOAL 120

QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTVTDALHVTSTVEG 174
DB 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTVTDALHVTSTVEG 174

RESULT 10
AAU72882
ID AAU72882 standard; protein; 234 AA.
XX AAU72882;
AC AAU72882;
XX 26-FEB-2002 (first entry)
DT Human aspartyl protease partial protein sequence #7.
XX Human aspartyl protease; cytosolic; immunomodulator; cardiant;
XX vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser;
KW hypertensive; neuroleptic; neuroprotective; anabolic;
KW anorectic; antiinflammatory; aspartyl protease; cysteine protease; colon;
KW metalloprotease; serine protease; cancer; haematopoietic; breast; pain;
KW lung; prostate; cervical; brain; ovarian; bladder; kidney; disease;
KW immune-related disease; cardiovascular disease; neuronal disease;
KW migraine; sexual dysfunction; mood disorder; attention disorder;
KW cognition disorder; hypotension; hypertension; psychotic disorder;
KW dyskinesia; metabolic disorder; inflammatory disorder.
XX Homo sapiens.
OS WO200183782-A2.
XX 08-NOV-2001.
PD 04-MAY-2001; 2001WO-US014431.
XX 04-MAY-2000; 2000US-0201879P.
PR (SUGE-) SUGEN INC.
XX Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI Payne V;
XX WPI; 2002-041502/05.
DR N-PSDB; AAS97165.
XX Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory disorders.
PT Claim 28; Fig 2A; 232pp; English.
XX The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoietic origin, of the breast, colon, lung, prostate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAU72876-AAU72910 represent human protease amino acid sequences of the invention

Sequence 234 AA;
Query Match 38.1%; Score 472.5; DB 5; Length 234;
Best Local Similarity 45.0%; Pred. NO. 8.1e-41;
Matches 107; Conservative 47; Mismatches 73; Indels 11; Gaps 7;

11 KYDMSGAALAILCVTKAREGSEEDLDALHMFROLRPFSTMKRDPRTAEQFOEELKFPQ 70
1 QYDLSKRAALLAVLQGRPGAGHVEALGGICWALGFETTVTRDPTAQAEELAQFRE 60
71 AIDSREDPVSCAFVLMMAH-GREGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVII 129
61 QLDTCRGPVSCALVALMAHGGPRGQLLGADGQEVQPEALMQELS--RCQVLQGRPKIFLL 118
130 QACRGQRDPGETVGGDEIVMWIK--DSPQTPTVTDALHVVSTVEGYIAYRHQKGSDF 187
119 QACRGGNRDAG--VGPTALPWTWSWLRAPPSVFSHADVLQIYAEAGGVAYR-DDKGSDF 175
188 IQTLVDVFTTKRGH-ILELLTEVTRMAEALVQE--GKARTNPEIOTSLKRLYLQ 242
176 IQTLVEVLNRPGRDLELLTEVNRVRCQEVGLGPCDCLKACLEIRSSLRRLCLQ 233

RESULT 11
BG76499
D ABG76499 standard; protein; 398 AA.

ABG76499;

05-NOV-2002 (first entry)

DNA encoding protein modification and maintenance molecule #3.

Protein modification and maintenance molecule; gastrointestinal disorder;
dysphagia; esophageal spasm; gastritis; anorexia; nausea; hypertension;
cardiovascular disorder; atherosclerosis; vasculitis; aneurysm; allergy;
ischemic heart disease; autoimmune disorder; inflammatory disorder;
acquired immunodeficiency syndrome; AIDS; ankylosing spondylitis; cancer;
anemia; amyloidosis; cell proliferative; arteriosclerotic burstis;
cirrhosis; developmental disorder; renal tubular acidosis; aneamia;
bone resorption; epilepsy; epithelial disorder; keratosis pilaris;
allergic contact dermatitis; insect bite; keloid; dermatofibroma; eczema;
neurological disorder; stroke; cerebral neoplasm; Alzheimer's disease;
Huntington's disease; dementia; reproductive disorder; infertility;
endometriosis; gynecomastia; ectopic pregnancy; gene therapy.

Homo sapiens.

WO200260942-A2.

08-AUG-2002.

30-JAN-2002; 2002WO-US002813.

31-JAN-2001; 2001US-0265705P.

05-FEB-2001; 2001US-0266762P.

16-FEB-2001; 2001US-0269581P.

23-FEB-2001; 2001US-0271198P.

01-MAR-2001; 2001US-0272813P.

13-MAR-2001; 2001US-0275586P.

23-MAR-2001; 2001US-0278505P.

30-MAR-2001; 2001US-0280539P.

(INCY-) INCYTE GENOMICS INC.

Warren BA, Honchell CD, Lu Y, Wallia NK, Burford N, Delegeane AM;

Gandhi AR, Baugun MR, Griffin JA, Gietzen KJ, Lu DM, Ison CH;

Rankumar J, Tang TY, Lal PG, Borowski M, Duggan BM, Hafalla AJA;

Arvizu C, Thangavelu X, Yao MG, Elliott VS, Ding L, Yue H, Lee S;

Swarnakar A, Tran UK, Xu Y;

WPI, 2002-608499/65.

N-P5DB; ABS59370.

New protein modification and maintenance molecules useful for treating or
preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
cell proliferative, developmental, neurological and reproductive
disorders.

Claim 1; Page 133-134; 172pp; English.

The invention describes an isolated human polypeptide (I), a naturally
occurring amino acid sequence at least 90 % identical to the protein, or
a biologically active fragment or an immunogenic fragment of the protein.
The protein modification and maintenance molecules are useful in the
diagnosis, treatment, and prevention of gastrointestinal (e.g. dysphagia,
esophageal spasm, gastritis, anorexia or nausea), cardiovascular (e.g.
atherosclerosis, hypertension, vasculitis, aneurysms, or ischaemic heart
disease), autoimmune/inflammatory (e.g. acquired immunodeficiency
syndrome (AIDS), allergies, ankylosing spondylitis, anaemia or
anlyoidosis), cell proliferative (e.g. cancers, arteriosclerotic,
burstis, or cirrhosis), developmental (e.g. renal tubular acidosis,
anemia, bone resorption, or epilepsy), epithelial (e.g. allergic contact
dermatitis, keratosis pilaris, insect bites, keloid, dermatofibroma or
eczema), neurological (e.g. stroke, cerebral neoplasms, Alzheimer's
disease), Huntington's disease or dementia), and reproductive disorders
(e.g. infertility, endometriosis, gynecomastia or ectopic pregnancy).
These may also be used in assessing the effects of exogenous compounds on
the expression of nucleic acid and amino acid sequences of protein
modification and maintenance molecules. Polynucleotides are useful in
somatic and germline gene therapy. This is the amino acid sequence of a
protein modification and maintenance molecule described in the invention
Sequence 398 AA;

Query Match 38.1%; Score 472.5; DB 5; Length 398;
Best Local Similarity 45.0%; Pred. No. 1.7e-40;
Matches 107; Conservative 47; Mismatches 73; Indels 11; Gaps 7;

QY 11 KYDMSGAALAILCVTKAREGSEEDLDALHMFROLRPFSTMKRDPRTAEQFOEELKFPQ 70
Db 165 QYDLSKRAALLAVLQGRPGAGHVEALGGICWALGFETTVTRDPTAQAEELAQFRE 224
QY 71 AIDSREDPVSCAFVLMMAH-GREGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVII 129
Db 225 QLDTCRGPVSCALVALMAHGGPRGQLLGADGQEVQPEALMQELS--RCQVLQGRPKIFLL 282
QY 130 QACRGQRDPGETVGGDEIVMWIK--DSPQTPTVTDALHVVSTVEGYIAYRHQKGSDF 187
Db 283 QACRGGNRDAG--VGPTALPWTWSWLRAPPSVFSHADVLQIYAEAGGVAYR-DDKGSDF 339
QY 188 IQTLVDVFTTKRGH-ILELLTEVTRMAEALVQE--GKARTNPEIOTSLKRLYLQ 242
Db 340 IQTLVEVLNRPGRDLELLTEVNRVRCQEVGLGPCDCLKACLEIRSSLRRLCLQ 397

RESULT 12

ABB10110

ID ABB10110 standard; protein; 452 AA.

AC ABB10110;

DT 26-JUL-2002 (first entry)

DE Mouse caspase 2 protein.

Caspase 2; antitense; cytostatic; osteopathic; cerebroprotective;
neuroprotective; antilipemic; antiinflammatory; antimicrobial;
haematopoietic disorder; bone metabolism disorder; cholesterol disorder;
hyperproliferative disorder; cancer; blood disorder; stroke;
brain injury; neurodegenerative disease; infection; inflammation; tumour.

Mus musculus.

WO200224720-A1.

28-MAR-2002.

14-SEP-2001; 2001WO-US028631.

20-SEP-2000; 2000US-00667018.

A (ISIS-) ISIS PHARM INC.

X Zhang H, Watt AT;

X WPI; 2002-351998/38.

R N-PSDB; ABB58563.

X New antisense compounds targeted to nucleic acid molecule encoding
T caspase 2, useful for treating diseases or conditions associated with
T caspase 2, e.g. cancer, blood disorders, stroke, brain injury and
T neurodegenerative diseases.

X Example 13; Page 111-113; 146pp; English.

X The invention relates to a compound 8-50 nucleobases in length targeted
C to a nucleic acid molecule encoding caspase 2, which specifically
C hybridises with and inhibits the expression of caspase 2, or specifically
C hybridises with at least an 8-nucleobase portion of an active site on a
C nucleic acid molecule encoding caspase 2. The activity of antisense
C oligonucleotides of the invention may be described as, cytostatic,
C osteopathic, cerebroprotective, neuroprotective, antilipemic,
C antiinflammatory and antimicrobial. The antisense compounds are useful
C for treating an animal having a disease or condition associated with
C caspase 2, such as haematopoietic disorder, bone metabolism disorder,
C cholesterol disorder, or a hyperproliferative disorder. These compounds
C may further be used as research reagents and diagnostics, to distinguish
C between functions of various members of a biological pathway, in the
C treatment of a disease or disorder which can be treated by modulating the
C expression of caspase 2, including cancer, blood disorders, stroke, brain
C injury and neurodegenerative diseases. They may also be used for tumour
C prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
C formation. The current sequence represents the mouse caspase 2 protein

X Sequence 452 AA;

Query Match 23.8%; Score 295; DB 5; Length 452;

Best Local Similarity 31.5%; Pred. No. 8.2e-22;

Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Y 29 REGSEEDLDALHMFRLQRFESTMKRDPATAEQFOELEKFOQAIDSRDVPSCAFVVLMA 88

b 219 RSGGDVHTTTLVTLFKLLGYNVHLVDQTAQEMQEKLNFAQ-LPAHRVTDSCV-VALLS 276

Y 89 HGREGLKGDGEWVKLENLFEALNNKCOALRAKPKVYIIQACRGEORDPG----- 140

b 277 HGVEGGIYVDGKLLQQLQGVFLFDNANCPSLQNKPMFFIOACRGDTRDGVDDQDGKN 336

Y 141 -----ETVGGDEIVMVKDSPTIPTYTDALHVSIVTEGYIAYRHDKGSCFIQTLV 192

b 337 HTQSPGCESDAGKEELMKMR-----LPTSDMICGYACKLGNAAAMNTKGSWYIEALT 391

Y 193 DVFTKR--KGHILELLTEVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241

b 392 QVFSERACDMHVADMLVKVNALIKE-----REGYAPGTFEHRCKEMSEYCSLCOQLYL 445

RESULT 13

ADB79812

ID ADB79812 standard; protein; 452 AA.

X ADB79812;

X 04-DEC-2003 (first entry)

X Rat caspase 2, Ich-1, SEQ ID 52.

X Analgesic; pain; streptozocin-induced diabetes; rat.

X Rattus norvegicus.

X EPI279744-A2.

X 29-JAN-2003.

XX

XX 26-JUL-2002; 2002EP-00255249.

XX 27-JUL-2001; 2001GB-00018354.

XX 07-FEB-2002; 2002GB-00002910.

XX (WARN) WARNER LAMBERT CO.

XX Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

XX WPI; 2003-395407/38.

XX N-PSDB; ADE79813.

XX Use of isolated gene sequences and encoded polypeptides that are
PT upregulated in the spinal cord in response to streptozocin-induced
PT diabetes for screening compounds for the treatment of pain, or for
PT diagnosing pain.

XX Claim 1; Page 115-117; 334pp; English.

XX The present invention relates to nucleotide sequences which are useful in
CC the screening of compounds for the treatment of pain, or for the
CC diagnosis of pain. The nucleotide sequences are up-regulated in the
CC spinal cord in response to streptozocin-induced diabetes. The present
CC sequence was used to illustrate the invention.

XX Sequence 452 AA;

Query Match 23.6%; Score 293; DB 7; Length 452;

Best Local Similarity 31.5%; Pred. No. 1.3e-21;

Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY 29 REGSEEDLDALHMFRLQRFESTMKRDPATAEQFOELEKFOQAIDSRDVPSCAFVVLMA 88

Db 219 RSGGDVHTTTLVTLFKLLGYNVHLVDQTAQEMQEKLNFAQ-LPAHRVTDSC-IVALLS 276

QY 89 HGREGLKGDGEWVKLENLFEALNNKCOALRAKPKVYIIQACRGEORDPG----- 140

Db 277 HGVEGGIYVDGKLLQQLQGVFLFDNANCPSLQNKPMFFIOACRGDTRDGVDDQDGKN 336

QY 141 -----ETVGGDEIVMVKDSPTIPTYTDALHVSIVTEGYIAYRHDKGSCFIQTLV 192

Db 337 HAQSPGCESDAGKEELMKMR-----LPTSDMICGYACKLGNAAAMNTKGSWYIEALT 391

QY 193 DVFTKR--KGHILELLTEVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241

Db 392 QVFSERACDMHVADMLVKVNALIKE-----REGYAPGTFEHRCKEMSEYCSLCOQLYL 445

RESULT 14

ADB63000

ID ADE63000 standard; protein; 452 AA.

XX ADE63000;

XX 29-JAN-2004 (first entry)

XX Rat Protein AAB96379, SEQ ID NO 8934.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEOH) GEN HOSPITAL CORP.
 2A (FARB) BAYER AG.
 XX
 21 Woolf C, D'urso D, Befort K, Costigan M;
 2R WPI; 2003-268312/26.
 2X GENBANK; AAB96379.
 2R
 2T New composition comprising two or more isolated polypeptides, useful for
 2T preparing a medicament for treating pain in an animal.
 2X
 2S Claim 1; Page; 1017pp; English.
 2X
 2X The invention discloses a composition comprising two or more isolated rat
 2X or human polynucleotides or a polynucleotide which represents a fragment,
 2X derivative or allelic variation of the nucleic acid sequence. Also
 2X claimed are a vector comprising the novel polynucleotide, a host cell
 2X comprising the vector, a method for identifying a nucleotide sequence
 2X which is differentially regulated in an animal subjected to pain and a
 2X kit to perform the method, an array, a method for identifying an agent
 2X that increases or decreases the expression of the polynucleotide sequence
 2X that is differentially expressed in neuronal tissue of a first animal
 2X subjected to pain, a method for identifying a compound which regulates
 2X the expression of a polynucleotide sequence which is differentially
 2X expressed in an animal subjected to pain, a method for identifying a
 2X compound that regulates the activity of one or more of the
 2X polynucleotides, a method for producing a pharmaceutical composition, a
 2X method for identifying a compound or small molecule that regulates the
 2X activity in an animal of one or more of the polypeptides given in the
 2X specification, a method for identifying a compound useful in treating
 2X pain and a pharmaceutical composition comprising the one or more
 2X polypeptides or their antibodies. The polynucleotide or the compound that
 2X modulates its activity is useful for preparing a medicament for treating
 2X pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 2X injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 2X therapy). The sequence presented is a rat protein (shown in Table 2 of
 2X the specification) which is differentially expressed during pain. Note:
 2X The sequence data for this patent did not form part of the printed
 2X specification, but was obtained in electronic form directly from WIPO at
 2X ftp.wipo.int/pub/published_pct_sequences.

3Q Sequence 452 AA;

Query Match 23.6%; Score 293; DB 7; Length 452;
 Best Local Similarity 31.5%; Pred. No. 1.3e-21;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;
 29 REGSEEDLDALEHMFRLQRFESTMKRDPTEAQFOBELEKFOQAIDSREDPVSCAFVVLMA 88
 219 RSGGDVHSTLTTLTKLLGVNVHLYDQTAQEMQKLNFAQ-LPAHRVTDSC-IVALLS 276
 89 HGREGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
 277 HGVEGGYIGVDGKLLQLOEVFRFDNANCPSLQNKPKMFFIQAACRGDETRGVQDQDGN 336
 141 -----ETVGGDEIVMWIKDSPQTIPTVTDALHVSIVTEGVIAYRHDKGSCFIQTLV 192
 337 HAQSPGCEESDAGKEMLMKR-----LPTSDMIGCYACLGKNAAMNTKRGSWVIALT 391
 193 DVFTKR--KGHILELLETVTRMAEAEVQSGKARKTN-----PEIQSTLRKRLYL 241
 392 QVFSERACDMHVADMLVKVNALIKE----REGYAPGTGFHRCKEMSEYCSLTCCQLYL 445

RESULT 15

AAR66771

D AAR66771 standard; protein; 435 AA.

X AAR66771;

X 25-MAR-2003 (revised)

T 13-SEP-1995 (first entry)

XX Human interleukin-1 beta converging enzyme ced 3 homolog Ich-1(L).
 DE
 XX
 2X Human interleukin-1 beta converging enzyme ced 3 homolog; Ich-1(L);
 2X oncogene bcl-2; programmed cell death; cancer treatment.
 2X
 2X Homo sapiens.
 2X
 2X Key Location/Qualifiers
 2X Active-site 301..305
 2X WO9500160-A1.
 2X
 2X OS-JAN-1995.
 2X
 2X 10-JUN-1994; 94MO-US006630.
 2X
 2X 24-JUN-1993; 93US-00080850.
 2X (GEOH) GEN HOSPITAL CORP.
 2X
 2X Yuan J, Miura M;
 2X WPI; 1995-051742/07.
 2X N-PSDB; AAR67971.
 2X
 2X or preventing programmed cell death in vertebrate cells - by inhibiting
 2X the activity of interleukin-1 beta converting enzyme.
 2X
 2X Example 5; Fig 12A; 116pp; English.
 2X
 2X AAR67971 encodes AAR66771 human interleukin-1 beta converting enzyme ced
 2X 3 homolog Ich-1(L), increasing Ich-1(L)s enzymatic activity can promote
 2X the programmed cell death of cancer cells (pref. those overexpressing the
 2X bcl-2 oncogene), this can be used as the basis of a new cancer treatment.
 2X Alternatively by reducing Ich-1(L)s enzymatic activity programmed cell
 2X death can be inhibited, this may be useful in the development of new cell
 2X lines which remain viable in culture for extended or indefinite periods,
 2X independent of growth factors. (Updated on 25-MAR-2003 to correct FN
 2X field.)

3Q Sequence 435 AA;

Query Match 23.3%; Score 289; DB 2; Length 435;
 Best Local Similarity 31.1%; Pred. No. 3.3e-21;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
 29 REGSEEDLDALEHMFRLQRFESTMKRDPTEAQFOBELEKFOQAIDSREDPVSCAFVVLMA 88
 202 RSGGDVHSTLTTLTKLLGVNVHLYDQTAQEMQKLNFAQ-LPAHRVTDSC-IVALLS 259
 89 HGREGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
 260 HGVEGGYIGVDGKLLQLOEVFRFDNANCPSLQNKPKMFFIQAACRGDETRGVQDQDGN 319
 141 -----ETVGGDEIVMWIKDSPQTIPTVTDALHVSIVTEGVIAYRHDKGSCFIQTLV 192
 320 HAQSPGCEESDAGKE-----LTPKRLPTRSDMIGCYACLGKNAAMNTKRGSWVIALA 374
 193 DVFTKR--KGHILELLETVTRMAEAEVQSGKARKTN-----PEIQSTLRKRLYL 241
 375 QVFSERACDMHVADMLVKVNALIKD----REGYAPGTGFHRCKEMSEYCSLTCCRLYL 428

Search completed: March 19, 2004, 11:22:15

Job time : 50.1713 secs